

FULL-LENGTH cDNA

FIELD OF THE INVENTION

The present invention relates to polynucleotides encoding
5 novel polypeptides, the polypeptides encoded by these
polynucleotides, and new uses of these.

BACKGROUND OF THE INVENTION

The genomic DNAs of various living organisms are currently
10 being sequenced and analyzed all over the world. The entire
genomic sequences of more than 40 species of prokaryotes, a
lower eukaryote, yeast, a multicellular eukaryote, *C. elegans*,
and a higher plant, *arabidopsis*, and such have already been
determined. Analysis of the human genome, presumed to have
15 three billion base pairs, was advanced under global cooperative
organization, and a draft sequence was disclosed in 2001. In
2003 the complete structure had been elucidated and publically
disclosed. A genome is a blueprint for highly complicated
living organisms. The aim in determining a genomic sequence is
20 to reveal the function and regulation of all genes, and to
understand living organisms as a network of interactions between
genes, proteins, cells or individuals. Understanding living
organisms through the genomic information of various species is
not only academically important, but also socially significant
25 from the viewpoint of industrial application.

However, simply determining a genomic sequence will not
reveal the function of all genes. For example, in the case of
yeast, the function of only approximately half of the 6000 genes
predicted on the basis of genomic sequence have been deduced.
30 The human genome has been estimated to contain about 30,000 to
40,000 genes. Further, 100,000 or more types of mRNAs are said
to exist when variants produced by alternative splicing are
taken into consideration. Therefore, it is desirable to
establish "a high throughput system for analysis of gene
35 functions" which allows rapid and efficient identification of

the functions of vast amounts of genes obtained by genomic sequencing.

Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to correctly predict the structure of an encoded protein based solely on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows easy identification of the protein's primary structure. In human cDNA research to date, more than three million ESTs (Expression Sequence Tags) are publicly available, which presumably covers no less than 80% of all human genes.

EST information is utilized in a variety of ways, for example in analyzing the structure of the human genome, or in predicting exon regions of genomic sequences or their expression profiles. However, most human ESTs have been derived from regions proximal to the cDNA 3'-end, and little information is available from around the mRNA 5'-end. In human cDNAs, the full-length protein sequence of approximately 15,000 corresponding mRNAs have been deduced.

It is possible to identify the mRNA transcription start site on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA contained in that sequence, or in the regulation of its expression at the translation stage. Also, since the atg codon, or translation start site, is contained in the 5'-region of a full-length cDNA, translation to proteins will occur in the correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA, or to analyze the biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of full-length cDNA provides valuable information which complements genome sequencing information. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

Therefore, if a novel human full-length cDNA can be isolated, it can be used for developing medicines for diseases in which its gene is involved. A protein encoded by such a gene can be used as a drug by itself. Thus, obtaining full-length cDNAs encoding novel human proteins is of great significance.

In particular, human secretory proteins or membrane proteins would be useful used as medicines in the same manner as tissue plasminogen activator (TPA), or as target proteins for medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, and such, are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

Isolating novel full-length human cDNA clones, only a few of which have been isolated, is of great significance. The isolation of novel cDNA clones encoding secretory proteins or membrane proteins is especially desired since such proteins would be useful in themselves as medicines, and also their clones would potentially include genes involved in disease. In addition, genes encoding proteins involved in signal transduction, glycoprotein, transcription, or disease, are expected to be useful as target molecules for therapy, or as medicines in themselves. These genes form a gene group predicted to be strongly involved in disease. Thus, identification of full-length cDNA clones encoding these proteins has great significance.

SUMMARY OF THE INVENTION

An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

The inventors have developed a method for efficiently cloning, from a cDNA library having a very high fullness-ratio, human full-length cDNAs predicted to be full-length cDNA clones,

where that cDNA library is synthesized by an improved method (WO 01/04286) of oligo-capping (K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)). The nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-end, and, if required, from their 3'-end.

Among the clones obtained, representative clones estimated to be novel and full-length were analyzed for their full-length nucleotide sequence. The determined full-length nucleotide sequences were analyzed using a BLAST homology search of the databases shown below. Homology searches of the present invention were carried out based on full-length cDNA information, including the entire coding region, and thus homology to every part of a polypeptide could be analyzed. Therefore, in the present invention, the reliability of homology searches has been greatly improved.

[1] SwissProt

(http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html),

[2] GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>),

[3] UniGene (Human) (<http://www.ncbi.nlm.nih.gov/UniGene>),

[4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (<http://www.rcsb.org/pdb/index.html>),

(<http://pir.georgetown.edu/pirwww/pirhome.shtml>), and PRF (<http://www.prf.or.jp/en/>); overlapping sequences have been removed.), and

[5] RefSeq (<http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>).

The gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

In the present invention, gene functions were revealed by analysis of expression profiles *in silico*, based on full-length

nucleotide sequence information. The expression profiles used in the expression frequency analysis were studied based on databases containing a sufficient amount of fragment sequence data. Expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of the many cDNA clones obtained in the present invention. Thus, highly reliable analysis was achieved by referring to the full-length nucleotide sequences of a wide variety of genes in a sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect gene expression frequency in tissues and cells from which a certain cDNA library was derived. Thus, the full-length cDNA nucleotide sequence information of the present invention made it possible to achieve highly reliable expression frequency analysis.

The full-length cDNA clones of the present invention were obtained by a method comprising the steps of [1] preparing libraries containing cDNAs with a high fullness ratio using oligo-capping, and [2] assembling 5'-end sequences and selecting those with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction). The use of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable full-length cDNAs to be readily obtained without using such special techniques. Primers, which are designed for use in obtaining cDNAs capable of being expressed, are not limited to the 5'- and 3'-end sequences of a polynucleotide.

Specifically, the present invention relates to polynucleotides and proteins encoded by the polypeptides as follows.

[1] A polynucleotide selected from the group consisting of:
(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence according to any one of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683;

(b) a polynucleotide comprising the nucleotide sequence encoding a polypeptide that comprises the amino acid sequence of any one of SEQ ID NOs: 2189-4376 and SEQ ID NOs: 4684-4990;

5 (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide, which comprises the amino acid sequence selected from SEQ ID NO: SEQ ID NOs: 2189-4376 and SEQ ID NOs: 4684-4990 wherein one or more amino acids have been substituted, deleted, inserted, and/or added, and which is functionally equivalent to the polypeptide comprising the selected amino acid
10 sequence as described above;

(d) a polynucleotide which hybridizes to a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683, and which comprises the nucleotide sequence encoding a polypeptide functionally
15 equivalent to a polypeptide encoded by the selected nucleotide sequence as described above;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotides according to any one of (a)-(d);

20 (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683; and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any
25 one of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683.

[2] A polypeptide encoded by the polynucleotide according to [1], or a partial peptide thereof.

[3] An antibody which binds to the polypeptide or the peptide according to [2].

30 [4] An immunoassay method for the polypeptide or the peptide according to [2], which comprises the steps of:

(a) contacting the polypeptide or the peptide according to [2] with the antibody according to [3]; and

(b) observing the binding between the two.

35 [5] A vector comprising the polynucleotide according to [1].

[6] A transformant comprising the polynucleotide according to [1] or the vector according to [5].

[7] A transformant which comprises the polynucleotide according to [1] or vector according to [5] in an expressible
5 manner.

[8] A method for producing the polypeptide or the peptide according to [2], which comprises the steps of:

(a) culturing the transformant according to [7]; and

(b) recovering the expression product.

10 [9] An oligonucleotide comprising 15 or more nucleotides, which comprises the nucleotide sequence according to any one of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683, or a nucleotide sequence complementary to the complementary strand thereof.

[10] A primer for synthesizing a polynucleotide, which
15 comprises the oligonucleotide according to [9].

[11] A probe for detecting a polynucleotide, which comprises the oligonucleotide according to [9].

[12] A polynucleotide according to any one of:

(a) an antisense polynucleotide comprising a nucleotide
20 sequence complementary to the transcript of the polynucleotide according to [1];

(b) a polynucleotide with the ribozyme activity for specifically cleaving the transcript of the polynucleotide according to [1]; and

25 (c) a polynucleotide which downregulates the expression of the polynucleotide of [1] due to RNAi activity in a host cell.

[13] A method for detecting the polynucleotide according to [1], which comprises the steps of:

(a) incubating a target polynucleotide with the
30 oligonucleotide according to [9] under conditions ensuring hybridization; and

(b) detecting the hybridization between the target polynucleotide and the oligonucleotide according to [9].

[14] A database of polynucleotides and/or polypeptides,
35 which comprises information on at least one of the nucleotide sequences of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683 and/or

on at least one of the amino acid sequences of SEQ ID NOs: 2189-4376 and SEQ ID NOs: 4684-4990.

Herein, "polynucleotide" is defined as a molecule, such as
5 a DNA or RNA, in which multiple nucleotides are polymerized. There is no limitation as to the number of polymerized nucleotides. If a polymer contains a relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention.
10 The polynucleotides or oligonucleotides of the present invention can be natural or chemically synthesized. Alternatively, they can be synthesized using a template polynucleotide in an enzymatic reaction such as PCR. Furthermore, the polynucleotides of the present invention may be modified
15 chemically. Single-stranded and double-stranded polynucleotides are included in the present invention. In this specification, especially in the claims, when the polynucleotides are described merely as "polynucleotide", it means not only single-stranded polynucleotides but also double-stranded polynucleotides. When
20 it means a double-stranded polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the corresponding complementary strand is essentially determined.

All the cDNAs provided by the present invention are full-
25 length cDNAs. "Full-length cDNAs" herein means cDNAs containing the ATG codon, which is the start point of translation therein. Untranslated regions upstream and downstream of the protein-coding region are both naturally contained in natural mRNAs and are not essential. It is preferable that the full-length cDNAs
30 of the present invention contain a stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the restriction map of the vector pME18SFL3.

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DETAILED DESCRIPTION OF THE INVENTION

All of the clones (2495 clones) of the present invention are novel and encode full-length polypeptides. Further, all of the clones are cDNAs with a high fullness ratio, and which were obtained by oligo-capping method. None of the clones are identical to any known human mRNAs (namely, they are novel clones) selected by searching 5'-end sequences and mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases using BLAST homology [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]. They are also clones that were assumed to have a higher fullness ratio among members in assembled clusters. Most of the clones with a high fullness ratio in a cluster had nucleotide sequences longer in the 5'-end direction.

All of the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on 5'-end and 3'-end sequences, or using primer sets of primers designed based on 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of 2,495 full-length cDNA clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rules set out in "DDBJ/EMBL/GenBank Feature Table Definition" (<http://www.ncbi.nlm.nih.gov/collab/FT/index.html>). The start position number corresponds to the first letter of "ATG", the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated by flanking with the mark "...". However, in clones without a stop codon, the termination position is indicated by the mark ">", according to the above rules.

Table 1

	3NB692002685	1	777.. 1496	2189
	3NB692002806	2	33.. 674	2190
5	3NB692008729	3	455.. 1189	2191
	ACTVT2000380	4	593.. 919	2192
	ADIPS2000088	5	59.. 1486	2193
	ADRGL2000172	6	237.. 638	2194
	ADRGL2003329	7	640.. 1014	2195
10	ADRGL2009146	8	313.. 732	2196
	ADRGL2009691	9	294.. 767	2197
	ADRGL2009755	10	87.. 1265	2198
	ADRGL2012038	11	342.. 686	2199
	ADRGL2012179	12	254.. 625	2200
15	ASTRO1000009	13	458.. 1552	2201
	ASTRO2002842	14	150.. 1490	2202
	ASTRO2003960	15	422.. 895	2203
	ASTRO2014923	16	65.. 1357	2204
	ASTRO2018373	17	123.. 512	2205
20	ASTRO3000172	18	2582.. 2890	2206
	ASTRO3000177	19	2311.. 3978	2207
	ASTRO3000301	20	125.. 3832	2208
	ASTRO3000482	21	90.. 557	2209
	BLADE1000176	22	1787.. 2101	2210
25	BLADE2001371	23	1009.. 1323	2211
	BLADE2001987	24	186.. 548	2212
	BLADE2002073	25	481.. 801	2213
	BLADE2002782	26	1341.. 1667	2214
	BLADE2002947	27	7.. 336	2215
30	BLADE2003474	28	967.. 1272	2216
	BLADE2004089	29	60.. >2486	2217
	BLADE2004462	30	96.. 512	2218
	BLADE2004670	31	2037.. >2574	2219
	BLADE2005036	32	1293.. 1838	2220
35	BLADE2005459	33	306.. 977	2221
	BLADE2007666	34	2289.. 2612	2222

	BLADE2007958	35	1147..1530	2223
	BLADE2008281	36	26.. 370	2224
	BLADE2008398	37	2742..3422	2225
	BLADE2008539	38	2857..4245	2226
5	BNGH42003570	39	98.. 802	2227
	BNGH42007788	40	472..1782	2228
	BRACE1000186	41	333.. 821	2229
	BRACE1000258	42	10..2538	2230
	BRACE1000533	43	1483..1908	2231
10	BRACE1000572	44	16..3435	2232
	BRACE2003639	45	481..1065	2233
	BRACE2005457	46	128..1237	2234
	BRACE2006319	47	603..1517	2235
	BRACE2008594	48	1221..1871	2236
15	BRACE2010489	49	262..>1693	2237
	BRACE2011747	50	983..1438	2238
	BRACE2014306	51	32..1402	2239
	BRACE2014475	52	598.. 906	2240
	BRACE2014657	53	404.. 814	2241
20	BRACE2015058	54	670..1116	2242
	BRACE2015314	55	203..1822	2243
	BRACE2016981	56	51..1355	2244
	BRACE2018762	57	654..1739	2245
	BRACE2024627	58	438.. 950	2246
25	BRACE2026836	59	134..1087	2247
	BRACE2027258	60	164..>1851	2248
	BRACE2027970	61	1538..1990	2249
	BRACE2028970	62	2257..2685	2250
	BRACE2029112	63	832..1191	2251
30	BRACE2029849	64	1039..1341	2252
	BRACE2030326	65	344.. 688	2253
	BRACE2030341	66	1209..1694	2254
	BRACE2030884	67	1248..1601	2255
	BRACE2031154	68	2.. 367	2256
35	BRACE2031389	69	690..1271	2257
	BRACE2031527	70	367.. 684	2258

	BRACE2031531	71	120.. 635	2259
	BRACE2031899	72	46.. 381	2260
	BRACE2032044	73	403.. 732	2261
	BRACE2032329	74	1330.. 1761	2262
5	BRACE2032385	75	20.. 613	2263
	BRACE2032538	76	189.. 515	2264
	BRACE2032823	77	1910.. 2212	2265
	BRACE2033720	78	28.. 537	2266
	BRACE2035381	79	1310.. 2758	2267
10	BRACE2035441	80	98.. 1660	2268
	BRACE2036005	81	1584.. 1913	2269
	BRACE2036096	82	1173.. 1484	2270
	BRACE2036830	83	391.. 702	2271
	BRACE2036834	84	1436.. 1894	2272
15	BRACE2037847	85	122.. 616	2273
	BRACE2038114	86	171.. 536	2274
	BRACE2038329	87	335.. 928	2275
	BRACE2038551	88	1913.. 2239	2276
	BRACE2039249	89	1085.. 1726	2277
20	BRACE2039327	90	361.. 1419	2278
	BRACE2039475	91	307.. 753	2279
	BRACE2039734	92	16.. >1730	2280
	BRACE2040138	93	797.. 1216	2281
	BRACE2040325	94	356.. 757	2282
25	BRACE2041009	95	29.. 1390	2283
	BRACE2041200	96	304.. 945	2284
	BRACE2041264	97	530.. 1105	2285
	BRACE2042550	98	15.. 1007	2286
	BRACE2043142	99	156.. 908	2287
30	BRACE2043248	100	1099.. 1581	2288
	BRACE2043349	101	202.. 531	2289
	BRACE2043665	102	858.. 1565	2290
	BRACE2044286	103	125.. 2011	2291
	BRACE2044816	104	188.. 670	2292
35	BRACE2044949	105	24.. 725	2293
	BRACE2045300	106	1174.. 1863	2294

	BRACE2045428	107	209.. 625	2295
	BRACE2045596	108	906.. 1583	2296
	BRACE2045772	109	31.. 777	2297
	BRACE2045947	110	499.. 1164	2298
5	BRACE2045954	111	1558.. 1863	2299
	BRACE2046251	112	527.. 1360	2300
	BRACE2046295	113	436.. 1428	2301
	BRACE2047011	114	1453.. 1794	2302
	BRACE2047350	115	2840.. 3487	2303
10	BRACE2047377	116	133.. 456	2304
	BRACE2047385	117	75.. 458	2305
	BRACE3000071	118	1729.. 2124	2306
	BRACE3000697	119	131.. 703	2307
	BRACE3000787	120	2208.. 2750	2308
15	BRACE3000840	121	564.. 3611	2309
	BRACE3000973	122	887.. 1666	2310
	BRACE3001002	123	292.. 624	2311
	BRACE3001217	124	2924.. 3241	2312
	BRACE3001391	125	1803.. 3506	2313
20	BRACE3001595	126	8.. 952	2314
	BRACE3001754	127	586.. 1188	2315
	BRACE3002298	128	67.. 375	2316
	BRACE3002390	129	136.. 537	2317
	BRACE3002508	130	3430.. 4104	2318
25	BRACE3003004	131	692.. 1027	2319
	BRACE3003192	132	1044.. 3245	2320
	BRACE3003595	133	1654.. 4179	2321
	BRACE3003698	134	506.. 847	2322
	BRACE3004058	135	2267.. 3040	2323
30	BRACE3004113	136	1887.. 2189	2324
	BRACE3004150	137	1537.. 2886	2325
	BRACE3004358	138	222.. 551	2326
	BRACE3004435	139	2782.. 3240	2327
	BRACE3004772	140	888.. 1577	2328
35	BRACE3004783	141	132.. 644	2329
	BRACE3004843	142	183.. 500	2330

	BRACE3004880	143	885..1655	2331
	BRACE3005145	144	717..1484	2332
	BRACE3005225	145	76.. 495	2333
	BRACE3005430	146	3120..3524	2334
5	BRACE3005499	147	205.. 531	2335
	BRACE3006185	148	220.. 648	2336
	BRACE3006226	149	580.. 951	2337
	BRACE3006462	150	1851..2213	2338
	BRACE3006872	151	1136..1957	2339
10	BRACE3007322	152	2918..>3227	2340
	BRACE3007472	153	190.. 573	2341
	BRACE3007480	154	93.. 962	2342
	BRACE3007559	155	1236..1592	2343
	BRACE3007625	156	36..3053	2344
15	BRACE3007642	157	1857..2294	2345
	BRACE3007767	158	237.. 758	2346
	BRACE3008036	159	162.. 512	2347
	BRACE3008092	160	3356..3724	2348
	BRACE3008137	161	208..3699	2349
20	BRACE3008384	162	123..1043	2350
	BRACE3008720	163	3014..3550	2351
	BRACE3008772	164	3900..4331	2352
	BRACE3009090	165	70.. 585	2353
	BRACE3009237	166	406.. 714	2354
25	BRACE3009297	167	2724..3107	2355
	BRACE3009377	168	1359..1790	2356
	BRACE3009574	169	180.. 527	2357
	BRACE3009701	170	1011..1550	2358
	BRACE3009708	171	105..2867	2359
30	BRACE3009724	172	2401..3282	2360
	BRACE3009747	173	2650..3171	2361
	BRACE3010397	174	1848..2660	2362
	BRACE3010428	175	269.. 628	2363
	BRACE3011271	176	689..1417	2364
35	BRACE3011421	177	372..3209	2365
	BRACE3011505	178	688..1035	2366

	BRACE3012364	179	1980..2633	2367
	BRACE3012930	180	1128..1718	2368
	BRACE3013119	181	66.. 395	2369
	BRACE3013576	182	2120..2971	2370
5	BRACE3013740	183	118.. 447	2371
	BRACE3013780	184	6..1124	2372
	BRACE3014005	185	1460..2374	2373
	BRACE3014068	186	29.. 373	2374
	BRACE3014231	187	928..1347	2375
10	BRACE3014317	188	44.. 550	2376
	BRACE3014807	189	144..1202	2377
	BRACE3015027	190	1..1656	2378
	BRACE3015121	191	3019..4404	2379
	BRACE3015262	192	27..2195	2380
15	BRACE3015521	193	2117..2827	2381
	BRACE3015894	194	285.. 773	2382
	BRACE3016884	195	303..2633	2383
	BRACE3018308	196	106.. 612	2384
	BRACE3018963	197	332.. 676	2385
20	BRACE3019055	198	1065..1940	2386
	BRACE3019084	199	1644..2369	2387
	BRACE3020194	200	1727..2161	2388
	BRACE3020286	201	85.. 426	2389
	BRACE3020594	202	250.. 624	2390
25	BRACE3022769	203	299.. 790	2391
	BRACE3023912	204	12.. 539	2392
	BRACE3024073	205	86.. 655	2393
	BRACE3024659	206	14.. 586	2394
	BRACE3024662	207	401.. 925	2395
30	BRACE3025153	208	98.. 523	2396
	BRACE3025457	209	1204..2541	2397
	BRACE3025531	210	1319..2338	2398
	BRACE3025630	211	1329..1919	2399
	BRACE3026008	212	250.. 558	2400
35	BRACE3026075	213	130.. 483	2401
	BRACE3026735	214	324.. 635	2402

	BRACE3027242	215	273.. 791	2403
	BRACE3027326	216	237.. 2372	2404
	BRACE3027478	217	32.. 529	2405
	BRACE3030103	218	320.. 682	2406
5	BRACE3031838	219	1661.. 1981	2407
	BRACE3032983	220	155.. 484	2408
	BRACE3040856	221	187.. 585	2409
	BRACE3045033	222	24.. 566	2410
	BRALZ2011796	223	132.. 1361	2411
10	BRALZ2012183	224	2172.. 2741	2412
	BRALZ2012848	225	218.. 754	2413
	BRALZ2014484	226	80.. 1411	2414
	BRALZ2016085	227	217.. >1672	2415
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15	BRALZ2017359	229	47.. 973	2417
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	NT2RI3000174	4516	18.. 2501	4823
	NT2RI3001132	4517	281.. 3265	4824
	NT2RI3002557	4518	3660.. >3975	4825
	NT2RI3005928	4519	1784.. 2194	4826
30	NT2RI3007167	4520	205.. 957	4827
	NT2RI3007443	4521	1024.. 3270	4828
	NT2RP7008435	4522	719.. 2437	4829
	NT2RP8000521	4523	635.. 1039	4830
	NTONG2008093	4524	81.. 635	4831
35	OCBBF2003327	4525	35.. 1516	4832
	OCBBF2005433	4526	154.. 2565	4833

	OCBBF2006987	4527	447..3125	4834
	OCBBF2008144	4528	375..>3049	4835
	OCBBF2009583	4529	443..1567	4836
	OCBBF2011669	4530	656..3346	4837
5	OCBBF2019684	4531	161..1555	4838
	OCBBF2020048	4532	109..1152	4839
	OCBBF2024284	4533	70..3063	4840
	OCBBF2030116	4534	445..2574	4841
	OCBBF2032274	4535	46..1053	4842
10	OCBBF2034637	4536	380..1897	4843
	OCBBF3000167	4537	139..1365	4844
	OCBBF3002654	4538	494..2284	4845
	OCBBF3003761	4539	316..2025	4846
	OCBBF3004972	4540	2394..3302	4847
15	PERIC2007068	4541	174..1523	4848
	PLACE7000333	4542	1736..2470	4849
	PLACE7000502	4543	2490..4577	4850
	PROST2000452	4544	1462..2097	4851
	PROST2009320	4545	1640..2221	4852
20	PROST2019487	4546	745..1149	4853
	PUAEN2006335	4547	123..1829	4854
	SKMUS2003194	4548	70..1317	4855
	SPLEN2004611	4549	1058..1651	4856
	SPLEN2016135	4550	70..699	4857
25	SPLEN2016781	4551	1665..2444	4858
	SPLEN2016932	4552	597..1079	4859
	SPLEN2030847	4553	101..931	4860
	SPLEN2033490	4554	1418..1897	4861
	SPLEN2036702	4555	122..2467	4862
30	SPLEN2037319	4556	20..364	4863
	SPLEN2039311	4557	343..768	4864
	SPLEN2039379	4558	4..2199	4865
	STOMA2003158	4559	593..1459	4866
	STOMA2004893	4560	1137..>1566	4867
35	SYNOV1000256	4561	2082..2927	4868
	SYNOV2001660	4562	917..1510	4869

	SYNOV2006620	4563	1036..1692	4870
	SYNOV2013637	4564	36..1085	4871
	SYNOV2021953	4565	375..1640	4872
	SYNOV4002744	4566	469..1302	4873
5	SYNOV4003981	4567	36..2837	4874
	SYNOV4005739	4568	1425..2075	4875
	SYNOV4005889	4569	79..2793	4876
	TBAES2000932	4570	1943..2437	4877
	TESOP2000390	4571	218..1651	4878
10	TESOP2001796	4572	129..1589	4879
	TESOP2005199	4573	108..1586	4880
	TESOP2006398	4574	2557..>3253	4881
	TESOP2006865	4575	-256..732	4882
	TESOP2007384	4576	168..1058	4883
15	TESTI1000266	4577	346..807	4884
	TESTI2008901	4578	432..2120	4885
	TESTI2015626	4579	448..1605	4886
	TESTI2025924	4580	163..2028	4887
	TESTI2026647	4581	753..1556	4888
20	TESTI2029252	4582	191..2293	4889
	TESTI2032643	4583	1810..2334	4890
	TESTI2034251	4584	188..>1827	4891
	TESTI2035981	4585	814..1155	4892
	TESTI2036288	4586	86..475	4893
25	TESTI2037830	4587	911..1228	4894
	TESTI2039060	4588	140..2080	4895
	TESTI2049956	4589	438..1856	4896
	TESTI2050780	4590	70..1470	4897
	TESTI4000137	4591	396..2435	4898
30	TESTI4000155	4592	72..3518	4899
	TESTI4000183	4593	258..1160	4900
	TESTI4000214	4594	60..3710	4901
	TESTI4000319	4595	1609..2916	4902
	TESTI4001984	4596	651..1166	4903
35	TESTI4005317	4597	607..2406	4904
	TESTI4006473	4598	166..4188	4905

	TESTI4008058	4599	849..2573	4906
	TESTI4008302	4600	933..2537	4907
	TESTI4010382	4601	160..4062	4908
	TESTI4011070	4602	978..>3811	4909
5	TESTI4011072	4603	255..>3737	4910
	TESTI4011829	4604	2254..>4540	4911
	TESTI4013365	4605	858..2717	4912
	TESTI4013602	4606	3496..3990	4913
	TESTI4013894	4607	367..1077	4914
10	TESTI4014801	4608	1383..2555	4915
	TESTI4015012	4609	1699..3558	4916
	TESTI4015442	4610	12..3323	4917
	TESTI4017714	4611	318..2501	4918
	TESTI4019657	4612	1789..2925	4919
15	TESTI4021482	4613	1..507	4920
	TESTI4024387	4614	404..1063	4921
	TESTI4025268	4615	3..1262	4922
	TESTI4025494	4616	282..2381	4923
	TESTI4025547	4617	5..964	4924
20	TESTI4025865	4618	45..1421	4925
	TESTI4026207	4619	96..2540	4926
	TESTI4028938	4620	200..1711	4927
	TESTI4028958	4621	1336..2502	4928
	TESTI4029348	4622	116..613	4929
25	TESTI4029528	4623	46..2544	4930
	TESTI4029690	4624	165..917	4931
	TESTI4031745	4625	1636..4002	4932
	TESTI4032090	4626	198..998	4933
	TESTI4032112	4627	815..1654	4934
30	TESTI4036767	4628	62..1039	4935
	TESTI4038721	4629	2156..3292	4936
	TESTI4041086	4630	1946..3313	4937
	TESTI4046240	4631	981..1469	4938
	THYMU2004139	4632	407..>2108	4939
35	THYMU2004284	4633	922..1344	4940
	THYMU2006001	4634	230..1663	4941

	THYMU2028739	4635	408.. 1925	4942
	THYMU2030462	4636	1324.. 1725	4943
	THYMU2031139	4637	382.. 1890	4944
	THYMU2031249	4638	643.. 1713	4945
5	THYMU2032976	4639	102.. 482	4946
	THYMU2033401	4640	221.. 646	4947
	THYMU2034279	4641	1718.. 2176	4948
	THYMU2035078	4642	396.. 902	4949
	THYMU2035710	4643	988.. 1443	4950
10	THYMU2040925	4644	179.. 727	4951
	THYMU3000269	4645	1966.. 2742	4952
	THYMU3000360	4646	792.. 1241	4953
	THYMU3001428	4647	486.. 2294	4954
	TKIDN2008778	4648	1512.. 1862	4955
15	TKIDN2012771	4649	2185.. 3315	4956
	TKIDN2018926	4650	59.. 388	4957
	TLIVE2001684	4651	1046.. 2137	4958
	TLIVE2002046	4652	255.. 1334	4959
	TLIVE2007607	4653	220.. 1746	4960
20	TRACH1000212	4654	32.. 3826	4961
	TRACH2000862	4655	259.. 2160	4962
	TRACH2007483	4656	756.. 3095	4963
	TRACH2019672	4657	289.. 1350	4964
	TRACH2024408	4658	392.. >2211	4965
25	TRACH2024559	4659	1450.. 1905	4966
	TRACH3000134	4660	293.. 2488	4967
	TRACH3000420	4661	17.. 3577	4968
	TRACH3002561	4662	2181.. 2603	4969
	TRACH3003683	4663	1157.. 1690	4970
30	TRACH3003832	4664	6.. 2798	4971
	TRACH3007866	4665	183.. 2450	4972
	TUTER2000057	4666	27.. 833	4973
	UTERU2004299	4667	452.. 934	4974
	UTERU2008040	4668	286.. 1521	4975
35	UTERU2011220	4669	453.. 842	4976
	UTERU2019534	4670	551.. 1021	4977

	UTERU2021820	4671	1545..2096	4978
	UTERU2028734	4672	217..1956	4979
	UTERU2032279	4673	1252..2037	4980
	UTERU2033577	4674	164..1009	4981
5	UTERU2035978	4675	56.. 436	4982
	UTERU3000402	4676	798..1598	4983
	UTERU3000738	4677	792..1547	4984
	UTERU3001053	4678	2485..>3535	4985
	UTERU3014791	4679	2452..3027	4986
10	UTERU3015069	4680	2538..3986	4987
	UTERU3015412	4681	67..1464	4988
	UTERU3017176	4682	3512..>3913	4989
	TEST14038779	4683	202..1971	4990

15 Primers used to synthesize polynucleotides can be designed
based on the nucleotide sequences of polynucleotides of the
present invention, shown in SEQ ID NOs in Table 1 above. When
synthesizing full-length cDNAs, an oligo dT primer can be used
as the 3'-end primer. The length of the primer is usually 15-
20 100 bp, and favorably between 15-35 bp. In the case of LA PCR,
described below, a primer length of 25-35 bp provides a good
result.

 Methods for designing a primer that enables specific
amplification based on a target nucleotide sequence are known to
25 those skilled in the art (Current Protocols in Molecular Biology,
Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4).
In principle, primers based on 5'-end sequences are designed
such that amplification products will include the translation
start site. Accordingly, for example, when the 5'-end primer is
30 designed based on the nucleotide sequence of the 5' untranslated
region (5'UTR), any part of the 5'-end, which ensures
specificity to the cDNA of interest, can be selected as the
primer.

 When synthesizing a full-length cDNA, the target nucleotide
35 sequence to be amplified can extend to several thousand bp in
some cDNA. Such long nucleotides can be amplified using methods

such as LA PCR (Long and Accurate PCR). The use of LA PCR is advantageous when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' → 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, amplification of nucleotides 20 kb or longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

Template DNAs for synthesizing the full-length cDNAs of the present invention can be obtained by using cDNA libraries prepared by various methods. The full-length cDNA clones of the present invention are clones with a high probability of completeness in length, obtained by a method comprising the steps of [1] preparing libraries containing cDNAs with a very high fullness ratio using oligo-capping, and [2] assembling 5'-end sequences and selecting those with the highest probability of completeness in length in clusters formed (there are many clones longer in the 5'-end direction).

However, the use of primers designed based on the full-length nucleotide sequences provided by the present invention enable full-length cDNAs to be easily obtained without using such a special technique.

The problem with commercially available cDNA libraries or those prepared by known methods is that mRNA contained in these libraries has a very low fullness ratio. Thus, it is difficult to screen full-length cDNA clones directly from the library using ordinary cloning methods. The present invention has revealed nucleotide sequences of novel full-length cDNA. If such a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to more reliably synthesize a full-length cDNA.

The present invention provides isolated polynucleotides comprising the nucleotide sequences of SEQ ID NO: 1 as shown in Table 1, or homologs thereof. As used herein, an "isolated polynucleotide" is a polynucleotide whose structure is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which comprises the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in DNA libraries such as cDNA or genomic DNA libraries.

The 5'-end sequence of the full-length cDNA clones of this invention can be used to isolate the regulatory elements of transcription, including the promoter on the genome. A rough draft of the human genome (an analysis of the human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence will be finished. However, using software to analyze transcription start sites on the human genome, in which long introns exist, is difficult. In contrast, it is easy to specify transcription start sites in the genomic sequence using nucleotide sequences which include the 5'-end of the full-length cDNA clones of the present invention, and thus it is easy to obtain genomic regions

involved in transcription regulation, which include promoters contained upstream of the transcription start site.

The polypeptides encoded by the full-length cDNAs of the invention can be prepared as recombinant polypeptides or as natural polypeptides. For example, a recombinant polypeptide can be prepared by inserting a polynucleotide encoding a polypeptide of the present invention into a vector, introducing the vector into an appropriate host cell, and purifying the polypeptide expressed within that transformed host cell, as described below. In contrast, a natural polypeptide can be prepared, for example, by utilizing an affinity column to which is attached an antibody against a polypeptide of the present invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19). The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (see, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing a polypeptide of the invention.

The present invention provides substantially pure proteins encoded by the full-length cDNAs of the present invention. The term "substantially pure" herein used in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities of the polypeptides of the present invention, clarified in the above-mentioned manner. Whether or not a particular polypeptide is functionally equivalent to a polypeptide of the present

invention can be verified by using the biological activity of the polypeptide of the present invention as an index to examine whether that polypeptide has the said activity.

Polypeptides functionally equivalent to polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into a polypeptide amino acid sequence (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5)).
Such polypeptides can also be generated by spontaneous mutations. The present invention also includes polypeptides comprising the amino acid sequences shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have a function equivalent to that of a polypeptide identified in the Examples of the present invention, described later.

There are no limitations as to the number and site of amino acid mutation, as long as polypeptide function is maintained. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, five amino acids, preferably four or three amino acids, more preferably two amino acids, and further preferably one amino acid.

Herein "conservative amino acid substitution" refers to substitution of an amino acid residue belonging to a group comprising a chemically similar side chain, with another amino acid in the same group. Groups of amino acid residues having similar side chains have been defined in the art. These groups include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine),

nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using hybridization (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to a polynucleotide encoding the polypeptide identified in the present Example, based on the identified nucleotide sequence (Table 1) or a portion thereof, and obtain a functionally equivalent polypeptide from the isolated polynucleotide. The present invention includes polypeptides encoded by polynucleotides which hybridize with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to those identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated include but are not limited to vertebrates such as humans, mice, rats, rabbits, pigs and cows.

Washing conditions for hybridization for polynucleotide isolation encoding functionally equivalent polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which hybridization is performed at "6x SSC, 40% Formamide, 25°C", and washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which hybridization is performed at "6x SSC, 40% Formamide, 37°C", and washing at "0.2x SSC, 55°C". Even more preferable are those in which hybridization is performed at "6x SSC, 50% Formamide,

37°C", and washing at "0.1x SSC, 62°C". The more stringent the hybridization conditions, the more frequently polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent
5 conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and washing at "0.2x SSC, 55°C".

One skilled in the art can suitably select various
10 conditions, such as SSC dilution ratio, formamide concentration, and temperature, to accomplish a similar stringency.

The above-mentioned combinations of SSC, SDS, and temperature conditions are indicated just as examples. Those skilled in the art can select hybridization conditions with
15 similar stringency to those mentioned above by properly combining the above-mentioned or other factors that determine hybridization stringency (for example, probe concentration, probe length, and duration of hybridization reaction).

The amino acid sequences of polypeptides isolated by using
20 hybridization techniques usually have high identity to those of the polypeptides of the present invention, shown in Table 1. The present invention encompasses polynucleotides comprising a nucleotide sequence with high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention
25 encompasses peptides, or polypeptides comprising an amino acid sequence with high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Even more
30 preferable is identity of 90% or more, 93% or more, or 95% or more. Further more preferable is 97% or more, or 99% or more. Identity can be determined using the BLAST search algorithm.

As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the BLAST algorithm of
35 Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and

BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, using for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, using
5 for example, score = 50, wordlength = 3. When utilizing the BLAST and Gapped BLAST programs, the default parameters of each program are used. See <http://www.ncbi.nlm.nih.gov>.

Using the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987)
10 John Wiley & Sons, Section 6.1-6.4)) and primers designed based on the nucleotide sequences (Table 1) or portions thereof as identified in the present Example, it is possible to isolate polynucleotide fragments highly homologous to the polynucleotide sequences or portions thereof, and to obtain polypeptides
15 functionally equivalent to a particular polypeptide identified in the present Example, based on the isolated polynucleotide fragment.

The present invention also provides polynucleotides containing at least 15 nucleotides complementary to a
20 polynucleotide comprising a nucleotide sequence of SEQ ID NOS shown in Table 1, or the complementary strand thereof. Herein, the term "complementary strand" is defined as the other strand to one strand of a double stranded DNA composed of A:T and G:C base pairs. In addition, "complementary" is not only defined as
25 sequences completely matching a continuous region of at least 15 nucleotides, but is also defined to include sequences comprising identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. Identity may be determined using the algorithm
30 described herein.

Such polynucleotides includes probes and primers used for the detection and amplification of polynucleotides encoding the inventive polypeptides. When used as a primer, such a polynucleotide usually comprises 15 to 100 bp, and preferably of
35 15 to 35 bp. When used as a probe, such a polynucleotide comprises the whole or a part of the sequence of a

polynucleotide of the present invention, and comprises at least 15 bp. When used as a primer, such a polynucleotide is complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

5 Furthermore, polynucleotides of the present invention include antisense polynucleotides for suppressing the expression of a polypeptide of the present invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp
10 or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or
15 abnormal expression). An antisense polynucleotide can be prepared, for example, using the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotides
20 encoding a polypeptide of this invention (for example, the nucleotide sequences of SEQ ID NOs: 1 to 2188 and SEQ ID NOs: 4377 to 4683).

The present invention also includes polynucleotides that can use ribozyme or RNA interference (RNAi) activity to
25 downregulate expression of a polynucleotide of the present invention, where such a polynucleotide can be designed based on the nucleotide sequence of the polynucleotide of the present invention.

A ribozyme is a polynucleotide that comprises 1) an
30 antisense sequence of a polynucleotide of the present invention, and 2) the nucleotide sequence of a catalytic unit required for catalytic action. The antisense sequence constituting the ribozyme can be appropriately selected to be compatible with the structure of the ribozyme's catalytic unit. The ribozyme's
35 catalytic unit is well known in the art. For example, the hammer-head ribozyme (Rossi et al. (1991) Pharmac. Ther. 50:

245-254) and hairpin ribozyme (Hampel et al. (1990) Nucl. Acids Res. 18: 299-304, and U.S. Pat. No. 5,254,678) are known to have nucleotide sequence-specific cleaving activity. These ribozymes use this catalytic activity to cleave, at a specific position, polynucleotides which hybridize to the antisense sequence.

For example, the autolytic domain of a hammer-head ribozyme cleaves on the 3' side of C15 in the sequence G13U14C15. Base pairing between U14 and A9 plays an important role in this activity, and A15 or U15 can be cleaved instead of C15 (Koizumi M, et al: FEBS Lett 228: 228, 1988). A restriction enzyme-like RNA-cleaving ribozyme that recognizes the target RNA sequences UC, UU, or UA can be produced by designing the ribozyme such that the substrate binding site complements the RNA sequence near the target site (Koizumi, M. et al., FEBS Lett, 239:285, 1988; Koizumi, M. and Otsuka, E., Protein, Nucleic acid, and Enzyme, 35:2191, 1990; Koizumi, M. et al., Nucl Acids Res, 17:7059, 1989). For example, the polynucleotides of the present invention (SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683) contain a number of potential target sites. The polynucleotides of the present invention can be cleaved at desired positions with a ribozyme which contains an appropriately selected antisense sequence.

The ribozyme preferably comprises RNA and may be synthesized chemically or produced by enzymatic reaction. Methods of chemical synthesizing RNA are known in the art. Alternatively, the ribozyme can be produced by using RNA polymerase to transcribe a polynucleotide encoding the ribozyme. To produce a ribozyme by transcription, a polynucleotide encoding the ribozyme is arranged downstream of a promotor recognized by an RNA polymerase. Such RNA polymerases include T7 RNA polymerase and SP6 RNA polymerase. Alternatively, a ribozyme can be expressed in a host cell by inserting a polynucleotide encoding the ribozyme into an appropriate vector, and then introducing the vector into a host cell. The vector contains a promotor that can direct the expression of the gene in the host cell.

The present invention also provides siRNA (small interfering RNA) that downregulates the expression of a polynucleotide of the present invention. siRNA is a technique for controlling gene expression that inhibits protein synthesis from an mRNA by using a double-stranded RNA which comprises the same nucleotide sequence as that mRNA (Fire et al. (1998) Nature 391: 806-811). The effect of downregulating gene expression using double-stranded RNA is called "the RNAi effect". siRNA has been reported to effectively control gene expression in mice (Zamore et al. (2000) Cell 101:25-33; Gura (2000) Nature 404: 804-808). Thus the introduction of such a double-stranded RNA into cells can result in selective downregulation of target gene expression.

There is no limitation as to the length of the siRNAs. The double-stranded RNAs introduced into cells are enzymatically digested inside these cells, starting from their original 3' end and forming fragments of 21 bp to 23 bp. The enzyme that digests the double-stranded RNA is called 'dicer'. The resulting double-stranded RNA fragments recognize and bind to target nucleotide sequences which comprise the same sequence. The nucleotide sequence is then cleaved by the activity of RNase III-like nuclease (Hammond et al. (2000) Nature, 404: 293-298; Zamore et al. (2000) Cell 101: 25-33).

siRNA is introduced into cells to downregulate gene expression using RNAi activity. siRNA can be introduced into cells using the same methods as for ribozymes. Specifically, chemically-synthesized, double-stranded RNA can be introduced into cells. When synthesized RNA, including antisense RNA and siRNA, is intended for introduction into cells, it can be pre-modified to prevent degradation by nuclease. For example, thiolated RNA is protected from nuclease degradation.

Alternatively, siRNA can be expressed in cells. For example, siRNA can be expressed in cells by inserting a sense sequence and its corresponding antisense sequence into a vector, and then transforming cells with that vector. When the two strands are adjacent, the expressed double-stranded RNA will

have a hairpin-loop structure. When the two strands are expressed under the control of different promoters, the resulting double-stranded RNA will comprise two separate strands. Promoters generally used for the expression of siRNA include the U6 promotor.

The nucleotide sequence of an antisense polynucleotide, ribozyme, or siRNA of the present invention may be completely identical or complementary to any one of the nucleotide sequences of SEQ ID NOs: 1-2188 and SEQ ID NOs: 4377-4683, or may have high homology to these nucleotide sequences. The phrase "high homology" to an antisense polynucleotide, ribozyme, or siRNA nucleotide sequence typically means 90% or higher homology, preferably 95% or higher homology, more preferably 98% or higher homology, and still more preferably 99% or higher homology. The homology of a nucleotide sequence can be estimated, for example, by a method described herein.

One skilled in the art can design siRNA based on the nucleotide sequence of a gene whose expression is to be downregulated. The typical methods for designing siRNA include, for example, those described below. To begin with, it is advantageous to avoid using as target sequences: 1) 5'- or 3'-untranslated regions, and 2) regions adjacent to the start codon.

These regions often serve as binding regions for transcriptional regulatory proteins. In addition, these regions may also contain nucleotide sequences conserved among various mRNAs, and thus they may act to inhibit the expression of genes other than the gene of interest.

Thus, it may be advantageous to arrange the target sequence, for example, within the ORF downstream of the start codon. It is preferable to adjust the number of nucleotides between the start codon and the target sequence, for example, to 50 nucleotides or more. Typically, the nucleotide sequence of an siRNA is designed so that it starts from an aa sequence and comprises 19-21 consecutive nucleotides. A dinucleotide overhang is added to one end of siRNA. The nucleotide sequence of such an overhang may include doublets, dTdT or UU sequences.

The GC content of a nucleotide sequence constituting siRNA is preferably about 50%. G and C nucleotide residues are preferably uniformly distributed throughout the siRNA.

5 The action of siRNA is based on sequence-specific mRNA hybridization. Thus, to achieve downregulation specific to a particular gene, it is essential to make the target nucleotide sequence as specific as possible to that gene. It is thus preferable to use homology searches to confirm that the proposed target nucleotide sequence exhibits negligible homology with
10 other genes. Nucleotide sequence homology can be determined using established algorithms.

As long as an siRNA of the present invention downregulates the expression of a polynucleotide of the present invention, it is not limited to nucleotide sequences obtained using the
15 typical design method described above. For example, even if the target sequence is not specific to the nucleotide sequence of a particular gene, it can specifically downregulate the expression of a gene of interest in cells which do not express genes comprising homologous nucleotide sequences. Furthermore,
20 double-stranded RNA having RNAi activity can be obtained without using the above-described methods typically used to select a target sequence.

The polynucleotides or antisense polynucleotides, ribozymes, and siRNAs of the present invention can be used in, for example,
25 gene therapy. Preferable target diseases may be, for example, cancers or various inflammatory diseases. Such molecules can be used for gene therapy, for example, by administering them to patients *in vivo* or *ex vivo* using viral vectors such as retroviral vectors, adenoviral vectors, and adeno-related viral
30 vectors, or non-viral vectors such as liposomes.

The present invention also includes partial peptides of the polypeptides of the invention. Such a partial peptide comprises a polypeptide generated as a result of removing a signal peptide from a secretory protein. If a polypeptide of the present
35 invention has activity as a receptor or ligand, the partial peptide may function as a competitive inhibitor of the

polypeptide, and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific to a polypeptide of the present invention, the peptides comprise at least seven amino acids, preferably eight amino acids or more, more preferably nine amino acids or more, and even more preferably ten amino acids or more. The peptide can be used to prepare an antibody against or competitive inhibitor of a polypeptide of the present invention, and can also be used to screen for a receptor that binds to the polypeptide of this invention. The partial peptides of this invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or by digesting a polypeptide of the invention with an appropriate peptidase.

The present invention also relates to a vector into which a polynucleotide of the invention is inserted. Vectors of the present invention are not limited as long as they can contain the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferred cloning vectors. To produce a polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert a polynucleotide of the present invention, ligation utilizing restriction sites can be performed according to standard methods (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

The GATEWAY™ system (Invitrogen), which is an expression vector construction system for polypeptide expression, can also be used (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-

specific recombinases (BP CLONASE™ and LR CLONASE™) derived from lambda phage and uses BP CLONASE™-specific recombination sites for the Entry Vector, and LR CLONASE™-specific recombination sites for the Destination Vector, which may comprise a tag
5 useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, a
10 second recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and efficiently. Using the above-mentioned typical restriction enzyme/ligase reaction
15 method, expression vector construction and expression of a polypeptide of interest takes about seven to ten days. However, using the GATEWAY™ system, the polypeptide of interest can be expressed and prepared in only three to four days. Thus, the system ensures a high-throughput functional analysis for
20 expressed polypeptides (<http://biotech.nikkeibp.co.jp/netlink/lto/gateway/>).

The present invention also relates to a transformant carrying a vector of the present invention. Any cell can be used as a host into which a vector of this invention is inserted,
25 and various kinds of host cells can be used depending on the purpose. For example, COS cells or CHO cells can be used for strong expression of the polypeptide in eukaryotic cells.

Introduction of such a vector into host cells can be performed, for example, by calcium phosphate precipitation,
30 electroporation (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection, etc.

Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the
35 polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1, or the complementary strand thereof, can

be used not only as a primer for synthesizing full-length cDNAs, but also for testing and diagnosing abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using a polynucleotide of this invention as a primer, a polynucleotide encoding a polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization, since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of sequence abnormality using RFLP analysis, SSCP, or sequencing. Where expression of an mRNA of the present invention varies according to a specific disease, analysis of the amount of mRNA expression using a polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of that disease.

The present invention also relates to antibodies that bind to a polypeptide of the present invention. There are no limitations as to the form of the antibodies of this invention. They include polyclonal antibodies, monoclonal antibodies, or portions thereof that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

A polyclonal antibody of this invention can be obtained according to the standard method of synthesizing an oligopeptide corresponding to an amino acid sequence, and immunizing rabbits with that peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). A monoclonal antibody of the present invention can be obtained according to the standard method of purifying a polypeptide expressed in *E. coli*, immunizing mice with that polypeptide, and producing a hybridoma cell by fusing spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

An antibody binding to a polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of abnormalities of the expression and structure of that polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and a polypeptide of this invention can then be detected for the above purpose using Western blotting, immunoprecipitation, or ELISA.

Furthermore, an antibody binding to a polypeptide of the present invention can be utilized for treating a disease associated with that polypeptide. If the antibody is used to treat patients, human antibodies, humanized antibodies, or chimeric antibodies are preferred due to their low antigenicity. Human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of a human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). These humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

The cDNAs (clones) of the present invention include polypeptide sequences encoding proteins whose function can be predicted, such as, for example, secretory and/or membrane proteins, glycoprotein-related proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, enzyme and/or metabolism-related proteins, cell division- and/or cell proliferation-related proteins, cytoskeleton-related proteins, nuclear protein and/or RNA synthesis-related proteins, protein synthesis and/or transport-related proteins, cellular defense-related proteins, development and/or differentiation-related proteins, DNA- and/or RNA-binding proteins, ATP- and/or GTP-binding proteins. The results of cDNA homology searches can be used to estimate whether a cDNA sequence comprises the function of an above-described protein. Specifically, the function of a polypeptide encoded by a cDNA of the present invention can be inferred by (a) searching for a

known gene or protein which is homologous to the complete or partial nucleotide sequence of the full-length cDNA of the present invention, and (b) comparing the function of the gene and that of the protein encoded by the gene.

5 Alternatively, the function of a polypeptide encoded by a cDNA of the present invention can be predicted when a signal sequence, transmembrane domain, nuclear translocation signal, glycosylation signal, phosphorylation site, zinc-finger motif, SH3 domain, or such is found in the amino acid sequence. In
10 particular, partial sequence structures such as motif and domain structures are commonly found in a number of proteins, and comprise a minimal functional protein structure. The Pfam database identifies a total of 4,832 types of motifs and domains, including both those whose functions have been clarified and
15 those whose functions remain unclear (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) Version 7.7 (the latest version as of December 2002).

A specific example of motif/domain function is shown below. The ITAM motif (immunoreceptor tyrosine-based activation motif)
20 is found in the intracellular region of the T cell receptor which is expressed on the cell membrane of T cells participating in an immune response (Flaswinkel, H. et al. Semin Immunol 1995 Feb,7(1):21-7). The ITAM motif has a tandem YXXL structure (tyrosine-arbitrary amino acid-arbitrary amino acid-leucine).
25 On extracellular stimulus by an antigen or antibody, the tyrosine in the motif is phosphorylated by an enzyme (LCK) with a kinase domain. Then, ZAP70 binds to the phosphorylated tyrosine via the SH2 domain, resulting in downstream signal transduction (Bu, J.Y. et al., Proc Natl Acad Sci U S A 1995 May
30 23, 92(11):5106-10; Neumeister, E.N. et al., Mol Cell Biol 1995 June, 15(6):3171-8).

A similar phenomenon has been found in mast cells as well as in T cells (Chen, T. et al., J Biol Chem 1996 Oct 11, 271(41):25308-15). Thus, at the molecular level, such a
35 phenomenon is the first step in the activation of immune cells

in immunologic diseases such as allergies, atopic dermatitis, and asthma.

Even in a simple exemplary scheme such as the one described above, there are three major motif/domain structures - ITAM, the SH2 domain, and the protein kinase domain - each of which play an important role. The mechanism of this scheme can be interpreted using these three structures. Thus, collecting, categorizing and elucidating the function of molecules that comprise common motif/domain structures is exceedingly important in understanding the molecular-based mechanisms of various cellular functions, including and in addition to the immune response described herein. Searching for motif/domain structures is highly important as the first step in elucidating the functions of unknown polypeptides. It is also understood that an entire polypeptide structure is comprised by minimal structures such as motifs and domains, thus providing the overall function of an entire polypeptide.

The overall function of a polypeptide in cells can be accurately predicted at the molecular level using data obtained by domain and motif structure analysis. In addition, a fusion polypeptide comprising a partial amino acid sequence and a GFP protein or the like may be prepared, and then introduced into cultured cells. For example, if a polypeptide is localized on the cell membrane, it may function as a receptor or ion channel. Alternatively, if a polypeptide is localized in the nucleus, it can be predicted to serve as a polynucleotide-binding protein or to participate in transcription. Thus, the function of a polypeptide can also be predicted by determining its localization.

The function of a full-length cDNA obtained in the present invention can be predicted by carrying out the above-described analysis using its entire nucleotide sequence and the amino acid sequence it encodes. Even when the full-length cDNA nucleotide sequence is not available, a partial sequence thereof (preferably 300 nucleotides or more) often enables function to be predicted. However, function predicted based on information

yielded in a partial sequence homology search will not necessarily be the same as that based on a full-length sequence. Functional prediction based on a full-length nucleotide sequence is obviously preferable.

5 A more specific method for predicting function involves homology searches of databases such as GenBank, Swiss-Prot, UniGene, nr and RefSeq, using BLAST or FASTA. The functions of polypeptides encoded by the cDNAs of the present invention can be predicted based on hit genes and the function of polypeptides
10 encoded by these genes. Polypeptide functions can be predicted from the amino acid sequences deduced from the structure of the full-length nucleotide sequences. In this way, signal sequences and transmembrane domains can be predicted from amino acid sequences using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:
15 897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14, 378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.), MEMSAT [D. T. Jones, W. R. Taylor & J. M. Thornton, Biochemistry, 33, 3038-3049 (1994)], and the like. Alternatively, motifs and domains can be predicted from amino acid sequences by carrying out
20 searches using Pfam, PROSITE (<http://www.expasy.ch/prosite/>), or such. The above-described procedures facilitate more accurate prediction of polypeptide function.

 The databases GenBank, Swiss-Prot, UniGene, nr and RefSeq were searched as described above for homology to the 2,495 full-
25 length clone sequences of the present invention whose full-length nucleotide had been determined (see Example 4 and the results of homology searches). In addition, the amino acid sequences deduced from the full-length nucleotide sequences were analyzed by database searches for signal sequences and
30 transmembrane domains using PSORT and SOSUI (see Example 5). The clones were categorized into the fourteen functional categories shown below, based on 1) the results of annotation-based functional prediction (by referring to keywords in the hit data of Swiss-Prot, or to Definitions and Reference information
35 in the hit data of GenBank, UniGene, nr or RefSeq), 2) the results of PSORT searches for signal sequences using the deduced

ORFs and 3) the results of SOSUI searches for transmembrane domains using the deduced ORFs. As a result, 1,229 clones were estimated to encode proteins belonging to the categories described below.

- 5 Secretory and/or membrane protein (741 clones)
 Glycoprotein-related protein (130 clones)
 Signal transduction-related protein (111 clones)
 Transcription-related protein (102 clones)
 Disease-related protein (426 clones)
- 10 Enzyme and/or metabolism-related protein (230 clones)
 Cell division- and/or cell proliferation-related protein (52 clones)
 Cytoskeleton-related protein (61 clones)
 Nuclear protein and/or RNA synthesis-related protein (58 clones)
- 15 Protein synthesis- and/or transport-related protein (72 clones)
 Cellular defense-related protein (seven clones)
 Development and/or differentiation-related protein (14 clones)
 DNA- and/or RNA-binding protein (129 clones)
 ATP- and/or GTP-binding protein (92 clones)
- 20 The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 659 clones.
 ACTVT2000380, ADIPS2000088, ADRGL2000172, ADRGL2003329,
 ADRGL2009146, ASTRO2014923, ASTRO3000301, BLADE1000176,
 BLADE2002073, BLADE2002947, BLADE2004462, BLADE2004670,
 25 BLADE2005036, BLADE2008539, BNGH42003570, BRACE1000186,
 BRACE2005457, BRACE2014306, BRACE2016981, BRACE2029112,
 BRACE2030884, BRACE2031527, BRACE2031531, BRACE2031899,
 BRACE2032385, BRACE2036005, BRACE2039249, BRACE2039327,
 BRACE2040138, BRACE2041200, BRACE2043142, BRACE2043665,
 30 BRACE2046295, BRACE3000697, BRACE3001391, BRACE3002298,
 BRACE3003004, BRACE3003595, BRACE3004058, BRACE3004113,
 BRACE3004772, BRACE3004843, BRACE3006462, BRACE3008137,
 BRACE3008384, BRACE3009574, BRACE3009708, BRACE3010397,
 BRACE3011271, BRACE3011505, BRACE3013740, BRACE3014005,
 35 BRACE3014068, BRACE3014807, BRACE3016884, BRACE3018963,
 BRACE3019084, BRACE3020286, BRACE3020594, BRACE3024662,

BRACE3025531, BRACE3025630, BRACE3026008, BRACE3026735,
 BRACE3027326, BRACE3031838, BRACE3040856, BRALZ2016085,
 BRAMY2001473, BRAMY2004771, BRAMY2005052, BRAMY2017528,
 BRAMY2019300, BRAMY2019963, BRAMY2021498, BRAMY2028856,
 5 BRAMY2033003, BRAMY2033116, BRAMY2033594, BRAMY2036396,
 BRAMY2039872, BRAMY2040592, BRAMY2041542, BRAMY2045036,
 BRAMY2047420, BRAMY2047751, BRAMY2047765, BRAMY3002312,
 BRAMY3004224, BRAMY3004919, BRAMY3007206, BRAMY3007609,
 BRAMY3008505, BRAMY4000095, BRASW1000125, BRAWH1000127,
 10 BRAWH2002560, BRAWH2002761, BRAWH2007658, BRAWH2014414,
 BRAWH2014954, BRAWH2016221, BRAWH2016439, BRAWH2016702,
 BRAWH3000078, BRAWH3000314, BRAWH3001475, BRAWH3001891,
 BRAWH3002600, BRAWH3003555, BRAWH3003727, BRAWH3003992,
 BRAWH3004453, BRAWH3004666, BRAWH3005132, BRAWH3005912,
 15 BRAWH3006548, BRAWH3007221, BRAWH3007506, BRAWH3007592,
 BRAWH3008634, BRCAN2002948, BRCAN2006063, BRCAN2009203,
 BRCAN2010376, BRCAN2012355, BRCAN2012481, BRCAN2013655,
 BRCAN2014143, BRCAN2016619, BRCAN2024451, BRCOC2007034,
 BRCOC2019934, BRHIP2000691, BRHIP2001805, BRHIP2002172,
 20 BRHIP2004814, BRHIP2004883, BRHIP2005236, BRHIP2005752,
 BRHIP2009414, BRHIP2013699, BRHIP2026288, BRHIP3000526,
 BRHIP3007483, BRHIP3007586, BRHIP3008598, BRHIP3009448,
 BRHIP3015751, BRHIP3024118, BRHIP3026097, BRSSN2003086,
 BRSSN2004496, BRSSN2008549, BRSSN2011738, BRSSN2014424,
 25 BRSSN2018925, BRSTN2000872, BRSTN2003835, BRSTN2007000,
 BRSTN2010363, BRSTN2012380, BRSTN2015015, BRSTN2016470,
 BRSTN2016678, BRSTN2017110, BRTHA2002376, BRTHA2002493,
 BRTHA2002608, BRTHA2002808, BRTHA2003110, BRTHA2003461,
 BRTHA2005579, BRTHA2006075, BRTHA2008527, BRTHA2011194,
 30 BRTHA2012980, BRTHA2013460, BRTHA2015696, BRTHA2015878,
 BRTHA2016215, BRTHA2016496, BRTHA2017985, BRTHA2018344,
 BRTHA2018624, BRTHA3000633, BRTHA3002427, BRTHA3003474,
 BRTHA3007148, BRTHA3008386, BRTHA3008778, BRTHA3009037,
 BRTHA3009090, BRTHA3009291, BRTHA3016845, BRTHA3017047,
 35 BRTHA3017589, BRTHA3017848, BRTHA3018656, CERVX2002006,
 COLON2000568, COLON2002443, COLON2004478, COLON2005126,

COLON2005772, CTONG1000302, CTONG1000341, CTONG1000488,
 CTONG1000508, CTONG2000042, CTONG2004062, CTONG2008233,
 CTONG2009423, CTONG2009531, CTONG2010803, CTONG2013178,
 CTONG2019652, CTONG2019788, CTONG2020127, CTONG2020522,
 5 CTONG2020638, CTONG2022601, CTONG2023512, CTONG2024749,
 CTONG2025496, CTONG2026920, CTONG2027327, CTONG2028124,
 CTONG2028687, CTONG3000707, CTONG3001370, CTONG3001560,
 CTONG3002020, CTONG3003179, CTONG3003483, CTONG3003737,
 CTONG3005648, CTONG3008252, CTONG3008258, CTONG3008496,
 10 CTONG3008566, CTONG3008951, CTONG3009227, CTONG3009239,
 CTONG3009328, CTONG3009385, D3OST2002182, D3OST2002648,
 DFNES1000107, DFNES2000146, DFNES2005266, DFNES2010502,
 FCBBF2001183, FCBBF2007510, FCBBF3003435, FCBBF3004502,
 FCBBF3009888, FCBBF3012170, FCBBF3021576, FCBBF3023895,
 15 FCBBF4000076, FEBRA1000030, FEBRA2007708, FEBRA2008311,
 FEBRA2008468, FEBRA2020668, FEBRA2025427, FEBRA2027082,
 HCASM2002502, HCASM2003212, HCASM2007047, HCHON2000212,
 HCHON2001084, HCHON2001548, HCHON2001577, HCHON2001712,
 HCHON2002676, HCHON2004007, HCHON2004776, HCHON2005921,
 20 HEART1000010, HEART2001680, HEART2010492, HLUNG2000014,
 HLUNG2003872, HLUNG2010464, HLUNG2015617, HLUNG2017350,
 HSYRA2005496, HSYRA2006873, HSYRA2008714, HSYRA2009102,
 IMR322002110, IMR322006222, KIDNE1000064, KIDNE2000832,
 KIDNE2000846, KIDNE2006580, KIDNE2010264, KIDNE2011635,
 25 KIDNE2012945, KIDNE2013095, LIVER2007415, LYMPB2000083,
 MESAN2001979, MESAN2012054, MESTC1000042, NHNPC2000606,
 NHNPC2001223, NOVAR2000136, NOVAR2001108, NT2RI2008724,
 NT2RI2009855, NT2RI2025909, NT2RI3001263, NT2RI3003095,
 NT2RI3003382, NT2RI3003409, NT2RI3005403, NT2RI3006171,
 30 NT2RI3006673, NT2RI3007065, NT2RI3007543, NT2RI3007978,
 NT2RP7000359, NT2RP7000466, NT2RP7004027, NT2RP7009030,
 NT2RP7014005, NTONG2000413, OCBBF2006151, OCBBF2006567,
 OCBBF2006764, OCBBF2007114, OCBBF2007428, OCBBF2009926,
 OCBBF2010140, OCBBF2017516, OCBBF2021788, OCBBF2024719,
 35 OCBBF2025458, OCBBF2030517, OCBBF2030574, OCBBF2031167,
 OCBBF2032590, OCBBF2033869, OCBBF2037598, OCBBF2038317,

OCBBF3000483, OCBBF3003320, OCBBF3004314, PEBLM2000170,
PEBLM2000338, PEBLM2002594, PEBLM2006113, PEBLM2007834,
PERIC2001227, PERIC2003452, PERIC2003720, PERIC2004909,
PERIC2005347, PERIC2006035, PERIC2007914, PLACE5000171,
5 PLACE5000260, PLACE5000282, PLACE6012574, PLACE6019932,
PLACE6020031, PLACE7000514, PLACE7001022, PROST1000184,
PROST1000528, PROST1000559, PROST2003428, PROST2018090,
PROST2018902, PROST2018922, PUAEN2002489, PUAEN2005588,
PUAEN2006701, PUAEN2009174, PUAEN2009795, RECTM2000433,
10 RECTM2001347, SKMUS2000757, SKNMC2002402, SMINT2002743,
SMINT2009902, SMINT2011888, SMINT2015787, SPLEN2001599,
SPLEN2009548, SPLEN2012889, SPLEN2015158, SPLEN2015267,
SPLEN2015679, SPLEN2021701, SPLEN2023733, SPLEN2023791,
SPLEN2025491, SPLEN2029522, SPLEN2029683, SPLEN2030335,
15 SPLEN2030479, SPLEN2031125, SPLEN2031424, SPLEN2031547,
SPLEN2031724, SPLEN2031780, SPLEN2032813, SPLEN2033098,
SPLEN2034021, SPLEN2034781, SPLEN2036326, SPLEN2036821,
SPLEN2037722, SPLEN2038180, SPLEN2038345, SPLEN2038407,
SPLEN2040222, SPLEN2041304, SPLEN2042598, STOMA2004294,
20 STOMA2008546, SYNOV2005817, SYNOV2012326, SYNOV2014400,
SYNOV2016124, SYNOV4002883, SYNOV4003322, SYNOV4004184,
SYNOV4004741, SYNOV4004914, SYNOV4006256, SYNOV4007430,
SYNOV4007553, SYNOV4007671, SYNOV4008336, SYNOV4008440,
TBAES2001258, TCERX2000613, TESOP2001345, TESOP2001865,
25 TESOP2002273, TESOP2002539, TESOP2004114, TESOP2005485,
TESOP2005579, TESOP2006041, TESOP2007052, TESOP2007262,
TESOP2007636, TESTI1000257, TESTI1000348, TESTI2000644,
TESTI2002036, TESTI2002618, TESTI2002928, TESTI2003347,
TESTI2005610, TESTI2006648, TESTI2013382, TESTI2024567,
30 TESTI2027019, TESTI2034767, TESTI2034953, TESTI2034997,
TESTI2035997, TESTI2036684, TESTI2042450, TESTI2047071,
TESTI2048898, TESTI2051767, TESTI2052822, TESTI4000215,
TESTI4000724, TESTI4001100, TESTI4001527, TESTI4001561,
TESTI4001665, TESTI4001923, TESTI4002552, TESTI4002754,
35 TESTI4005805, TESTI4005961, TESTI4006053, TESTI4006137,
TESTI4007064, TESTI4007163, TESTI4007239, TESTI4007382,

TESTI4008050, TESTI4008401, TESTI4008429, TESTI4008797,
TESTI4009608, TESTI4012448, TESTI4013369, TESTI4013667,
TESTI4013830, TESTI4014392, TESTI4016238, TESTI4017575,
TESTI4017901, TESTI4018835, TESTI4019566, TESTI4020092,
5 TESTI4020102, TESTI4021478, TESTI4023722, TESTI4024420,
TESTI4024874, TESTI4024890, TESTI4025797, TESTI4026456,
TESTI4026785, TESTI4027821, TESTI4028062, TESTI4028429,
TESTI4028823, TESTI4028880, TESTI4029836, TESTI4030159,
TESTI4030505, TESTI4034172, TESTI4035065, TESTI4035649,
10 TESTI4037244, TESTI4041053, TESTI4042711, TESTI4046487,
TESTI4046819, THYMU2001053, THYMU2003632, THYMU2003760,
THYMU2005003, THYMU2005303, THYMU2005321, THYMU2007658,
THYMU2008725, THYMU2009425, THYMU2011548, THYMU2013386,
THYMU2014353, THYMU2019210, THYMU2023711, THYMU2027497,
15 THYMU2027695, THYMU2029676, THYMU2030068, THYMU2032035,
THYMU2032437, THYMU2032655, THYMU2033079, THYMU2033308,
THYMU2033816, THYMU2034314, THYMU2035064, THYMU2036085,
THYMU2036459, THYMU2037226, THYMU2037348, THYMU2038772,
THYMU2038797, THYMU2039780, THYMU2040412, THYMU2041015,
20 THYMU3000028, THYMU3000036, THYMU3004835, THYMU3005696,
THYMU3006168, THYMU3006811, THYMU3007137, THYMU3007368,
THYMU3007845, TKIDN2002424, TKIDN2002632, TKIDN2006525,
TKIDN2009092, TKIDN2009889, TKIDN2014771, TKIDN2019116,
TLIVE2000023, TLIVE2001828, TLIVE2001927, TLIVE2002336,
25 TLIVE2002690, TLIVE2003381, TLIVE2004110, TLIVE2008229,
TOVAR2001281, TRACH1000205, TRACH2001549, TRACH2001684,
TRACH2006387, TRACH2007059, TRACH2007834, TRACH2008300,
TRACH2020525, TRACH2021964, TRACH2022553, TRACH2025535,
TRACH2025911, TRACH3000014, TRACH3002064, TRACH3002168,
30 TRACH3002650, TRACH3004786, TRACH3005294, TRACH3005549,
TRACH3006149, TRACH3007391, TRACH3008629, TRACH3035199,
TRACH3035526, TRACH3036193, TSTOM2000442, TSTOM2000553,
TUTER2000916, UTERU1000339, UTERU2004688, UTERU2004929,
UTERU2006137, UTERU2006568, UTERU2007444, UTERU2017762,
35 UTERU2020718, UTERU2022020, UTERU2025025, UTERU2025645,
UTERU2025891, UTERU2026090, UTERU2026203, UTERU2027591,

UTERU2029953, UTERU2031851, UTERU2035323, UTERU2035469,
 UTERU3000645, UTERU3000899, UTERU3001240, UTERU3001571,
 UTERU3001585, UTERU3001652, UTERU3001988, UTERU3002209,
 UTERU3002383, UTERU3002786, UTERU3003116, UTERU3003776,
 5 UTERU3006308, UTERU3008671, UTERU3009690, UTERU3009979,
 UTERU3011063, UTERU3015500, UTERU3016789

The following 82 clones are also predicted to belong to the category of secretory protein and/or membrane protein.

BLADE2006830, BRACE2002589, BRACE2009318, BRACE2011677,
 10 BRACE2029396, BRACE2039823, BRACE2039832, BRAMY2019111,
 BRAMY2038516, BRAMY2045471, BRAWH2006395, BRAWH2008993,
 BRCOC2019841, BRHIP2003272, BRHIP2005271, BRHIP2005724,
 BRHIP2008389, BRHIP2026877, BRHIP3000240, BRTHA2011321,
 BRTHA2018011, BRTHA2018443, BRTHA3008826, CTONG2015633,
 15 CTONG2016942, CTONG2019822, FEBRA2000790, FEBRA2006519,
 FEBRA2028256, FEBRA2028516, HCASM2002754, HEART2009680,
 HLUNG2013350, HLUNG2015418, IMR322013396, LIVER2000247,
 NT2RI2009583, NT2RI2027157, NT2RP7008435, OCBBF2003327,
 OCBBF2030116, PLACE7000502, PROST2000452, PROST2019487,
 20 SPLEN2016932, SPLEN2037319, SYNOV2001660, SYNOV2013637,
 SYNOV4003981, SYNOV4005889, TBAES2000932, TESTI2015626,
 TESTI2029252, TESTI2032643, TESTI2039060, TESTI2050780,
 TESTI4000137, TESTI4000155, TESTI4006473, TESTI4011070,
 TESTI4013365, TESTI4013894, TESTI4014801, TESTI4032090,
 25 TESTI4041086, THYMU2004284, THYMU2030462, THYMU2033401,
 THYMU2034279, THYMU2035710, THYMU2040925, TKIDN2008778,
 TKIDN2012771, TKIDN2018926, TLIVE2007607, TRACH2019672,
 TRACH3000420, TRACH3003683, UTERU2011220, UTERU2021820,
 UTERU2032279, UTERU3015069

30 The clones predicted to belong to the category of glycoprotein-related protein are the following 115 clones.

ADIPS2000088, BNGH42003570, BRACE2005457, BRACE2014306,
 BRACE2029112, BRACE2039249, BRACE2046295, BRACE3001391,
 BRACE3011271, BRACE3016884, BRAMY2005052, BRAMY3004919,
 35 BRAMY4000095, BRAMY4000277, BRAWH1000127, BRAWH2007658,
 BRAWH2014414, BRAWH2016221, BRAWH3002600, BRCAN2006063,

BRSSN2004496, BRTHA2008527, BRTHA2012980, BRTHA2016496,
 BRTHA3002427, BRTHA3017848, COLON2000568, COLON2004478,
 COLON2005772, CTONG1000341, CTONG2000042, CTONG2009423,
 CTONG2023512, CTONG2024749, CTONG2025496, CTONG3001370,
 5 CTONG3003737, D3OST2002648, DFNES2000146, DFNES2005266,
 FCBBF3012170, FEBRA1000030, FEBRA2008311, FEBRA2008468,
 HCHON2001712, HEART1000010, HEART2001680, HSYRA2005496,
 KIDNE2012945, LYMPB2000083, NESOP2001433, NOVAR2000136,
 NOVAR2001108, NT2RI3006171, NT2RI3006673, NT2RP7004027,
 10 OCBBF2033869, PLACE5000171, PROST1000184, PUAEN2009795,
 SMINT2010076, SMINT2011888, SMINT2015787, SPLEN2015267,
 SPLEN2021701, SPLEN2030335, SYNOV2005817, SYNOV2014400,
 SYNOV3000231, SYNOV3000302, TESOP2004114, TESOP2005485,
 TESTI1000257, TESTI2002036, TESTI2002618, TESTI2024567,
 15 TESTI2027019, TESTI4001527, TESTI4007163, TESTI4012406,
 TESTI4013830, TESTI4020092, TESTI4023546, TESTI4028823,
 TESTI4028880, TESTI4046819, THYMU2005303, THYMU2008725,
 THYMU2009425, THYMU2011548, THYMU2019210, THYMU2023711,
 THYMU2027497, THYMU2027695, THYMU2038797, THYMU3004835,
 20 TLIVE2003381, TRACH2006387, TRACH2007059, TRACH2022425,
 TRACH2022553, TRACH2022649, TRACH3002168, TRACH3008629,
 TRACH3035526, TSTOM2000442, UTERU2008347, UTERU2025025,
 UTERU2035469, UTERU3000899, UTERU3001240, UTERU3003116,
 UTERU3006308, UTERU3008671, UTERU3015500

25 The following 15 clones are also predicted to belong to the
 category of glycoprotein-related protein.

BRAMY2019111, BRHIP2026877, BRTHA2018011, FEBRA2028256,
 HEART2009680, HLUNG2015418, NT2RI2009583, NT2RP7008435,
 OCBBF2003327, TESTI2032643, TESTI2039060, TESTI4011070,
 30 THYMU2035710, TRACH3003683, UTERU2032279

 The clones predicted to belong to the category of signal
 transduction-related protein are the following 80 clones.

BNGH42007788, BRACE2008594, BRACE2030341, BRACE2044286,
 BRACE3002508, BRACE3003595, BRACE3006872, BRACE3011421,
 35 BRACE3015027, BRACE3027326, BRAMY2036567, BRAMY2038904,
 BRAMY3000213, BRAMY3002803, BRAMY3005091, BRAMY3005932,

BRAMY4000095, BRAMY4000229, BRCAN2003703, BRCAN2014602,
 BRCAN2016619, BRCAN2028355, BRHIP2000819, BRHIP3025161,
 BRSSN2004719, BRSTN2008418, BRTHA2002281, BRTHA2015406,
 CTONG2006798, CTONG3000084, CTONG3002412, D3OST3000169,
 5 FCBBF3007540, HCASM2001301, HCHON2006250, HCHON2008112,
 HLUNG2002465, KIDNE2001847, NESOP2001694, NT2NE2003252,
 NT2RI2005166, NT2RI3007757, NT2RI3008652, NT2RP7005529,
 NT2RP7009147, NT2RP7013795, NT2RP8000483, OCBBF2004826,
 OCBBF2007028, OCBBF2022351, OCBBF2030354, OCBBF2037547,
 10 PLACE6019385, PLACE7008431, PROST2016462, PROST2018511,
 PUAEN2009852, SPLEN2036932, SYNOV2021320, TESOP2000801,
 TESOP2001166, TESTI2005739, TESTI2026505, TESTI2050137,
 TESTI4011745, TESTI4012505, TESTI4018208, TESTI4028059,
 THYMU2007060, THYMU2031046, THYMU2032014, THYMU2039305,
 15 THYMU3008436, TLIVE2001327, TRACH2009310, TRACH2025535,
 TRACH3009455, UTERU2025025, UTERU2036089, UTERU3016789

The following 31 clones are also predicted to belong to the category of signal transduction-related protein.

BRAMY3004800, BRAWH3009017, BRHIP2026877, BRTHA2013610,
 20 BRTHA2017972, BRTHA3003000, CTONG2020974, FEBRA2001990,
 FEBRA2008692, NT2RI2005772, NT2RI3007443, NTONG2008093,
 OCBBF2005433, OCBBF2024284, OCBBF2034637, OCBBF3002654,
 SPLEN2036702, SPLEN2039379, TESOP2000390, TESTI2025924,
 TESTI2049956, TESTI4000319, TESTI4019657, TESTI4021482,
 25 TESTI4024387, TESTI4025268, TESTI4031745, THYMU2004139,
 THYMU2031249, UTERU2008040, UTERU3000738

The clones predicted to belong to the category of transcription-related protein are the following 38 clones.

BRACE2030326, BRACE3001002, BRACE3045033, BRHIP3025161,
 30 BRSSN2014299, BRTHA2014792, BRTHA3001721, CTONG2025516,
 FEBRA2007544, FEBRA2007801, HEART1000074, IMR322000127,
 IMR322000917, NT2NE2006531, NT2RI2006686, NT2RI3009158,
 OCBBF2020838, OCBBF2036743, PEBLM2002887, SKNMC2007504,
 SPLEN2012624, TESTI2026505, TESTI2040018, TESTI2044796,
 35 TESTI2050987, TESTI4001176, TESTI4007810, TESTI4014175,
 TESTI4017543, TESTI4026524, TESTI4036909, THYMU2006420,

THYMU2037233, THYMU3004866, TRACH3000558, TUTER2000425,
UTERU2035328, UTERU3009490

The following 64 clones are also predicted to belong to the category of transcription-related protein.

5 BRACE2003609, BRACE3001058, BRACE3001113, BRALZ2017844,
BRAMY2035070, BRAMY2035449, BRAMY2035718, BRAMY2039341,
BRAWH2006207, BRHIP2017553, CERVX2002013, CTONG1000113,
CTONG2003348, CTONG2008721, CTONG2020378, CTONG2020411,
CTONG2028758, CTONG3004726, DFNES2011192, FCBBF3010361,
10 FEBRA2014122, FEBRA2027609, HCASM2003018, HCHON2004858,
HSYRA2005628, MESAN2005303, MESAN2014412, MESAN2015501,
NT2RI2008952, NT2RI2018448, NT2RI3001132, OCBBF2008144,
OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2032274,
OCBBF3000167, SPLEN2004611, SPLEN2016135, SPLEN2016781,
15 SYNOV2021953, SYNOV4002744, TESOP2001796, TESOP2005199,
TESOP2006398, TESOP2006865, TESTI2034251, TESTI4000183,
TESTI4000214, TESTI4008302, TESTI4015442, TESTI4025494,
TESTI4025547, TESTI4028938, TESTI4032112, THYMU2006001,
THYMU2028739, TRACH2007483, TRACH3000134, TRACH3003832,
20 TUTER2000057, UTERU2033577, UTERU3001053, TESTI4038779

The clones predicted to belong to the category of disease-related protein are the following 342 clones.

3NB692002806, ADIPS2000088, BLADE2005036, BRACE2005457,
BRACE2008594, BRACE2014306, BRACE2016981, BRACE2018762,
25 BRACE2035381, BRACE2038551, BRACE2039249, BRACE2045300,
BRACE3000840, BRACE3001002, BRACE3001391, BRACE3001754,
BRACE3002508, BRACE3003595, BRACE3004058, BRACE3004150,
BRACE3004772, BRACE3008137, BRACE3008384, BRACE3009708,
BRACE3010397, BRACE3011271, BRACE3011421, BRACE3014807,
30 BRACE3015027, BRACE3015521, BRACE3018963, BRACE3020594,
BRACE3027326, BRALZ2017359, BRAMY2005052, BRAMY2038904,
BRAMY2047751, BRAMY3000213, BRAMY3005091, BRAMY3007609,
BRAMY4000095, BRAMY4000229, BRAMY4000277, BRAWH2001395,
BRAWH2002560, BRAWH2010000, BRAWH2010536, BRAWH2014414,
35 BRAWH3000100, BRAWH3000491, BRAWH3001326, BRAWH3002574,
BRAWH3005912, BRAWH3008341, BRCAN2002562, BRCAN2002856,

BRCAN2002948, BRCAN2003746, BRCAN2006063, BRCAN2009203,
 BRCAN2014602, BRCAN2016619, BRCAN2017442, BRCAN2024451,
 BRCOC2001505, BRCOC2003213, BRHIP2000819, BRHIP2001805,
 BRHIP2009414, BRHIP2024165, BRHIP2026288, BRHIP3000339,
 5 BRHIP3008405, BRHIP3009448, BRHIP3027137, BRHIP3027854,
 BRSSN2000684, BRSSN2004719, BRSSN2014424, BRSTN2001613,
 BRSTN2004987, BRSTN2008418, BRTHA2002608, BRTHA2003110,
 BRTHA2007122, BRTHA2007603, BRTHA2008527, BRTHA2012980,
 BRTHA2014792, BRTHA3001721, BRTHA3002427, BRTHA3003074,
 10 BRTHA3003449, BRTHA3008778, BRTHA3009037, BRTHA3009090,
 BRTHA3015815, BRTHA3016917, BRTHA3017848, COLON2000568,
 COLON2002520, CTONG1000341, CTONG2000042, CTONG2009423,
 CTONG2010803, CTONG2017500, CTONG2023021, CTONG2025496,
 CTONG2025516, CTONG3000084, CTONG3002412, CTONG3008639,
 15 D3OST2002182, D3OST2002648, DFNES2001108, FCBBF3009888,
 FEBRA2007708, FEBRA2008468, FEBRA2024744, HCASM2001301,
 HCASM2007737, HCHON2001712, HCHON2002676, HCHON2003532,
 HCHON2004007, HCHON2004531, HCHON2008112, HCHON2008444,
 HEART1000010, HEART1000139, HEART2001680, HEART2010495,
 20 HLUNG2002465, HSYRA2005496, IMR322000127, IMR322001380,
 IMR322006495, KIDNE2001847, KIDNE2012945, NESOP2001694,
 NOVAR2001108, NT2NE2003252, NT2NE2006531, NT2NE2006909,
 NT2RI2006686, NT2RI2025909, NT2RI3001515, NT2RI3006171,
 NT2RI3006340, NT2RI3006673, NT2RI3007757, NT2RI3008652,
 25 NT2RP7000359, NT2RP7005118, NT2RP7005529, NT2RP7010599,
 NTONG2000413, OCBBF2006058, OCBBF2020801, OCBBF2021788,
 OCBBF2031167, OCBBF2033869, OCBBF2036743, OCBBF2037068,
 OCBBF2037340, OCBBF3003320, PEBLM2000170, PEBLM2002887,
 PERIC2003720, PERIC2007914, PERIC2008385, PERIC2009086,
 30 PLACE5000282, PLACE6019385, PROST1000184, PROST2003428,
 PROST2016462, PROST2017367, PROST2018090, PROST2018511,
 PUAEN2002489, PUAEN2009795, SKNMC2007504, SMINT2010076,
 SPLEN2002467, SPLEN2006122, SPLEN2011422, SPLEN2012624,
 SPLEN2021701, SPLEN2031547, SPLEN2033098, SPLEN2036326,
 35 SPLEN2036821, SPLEN2036932, SYNOV2005817, SYNOV2012326,
 SYNOV2014400, SYNOV2021320, SYNOV3000231, SYNOV3000302,

SYNOV4002883, SYNOV4004741, SYNOV4007360, SYNOV4007521,
 SYNOV4007553, SYNOV4007671, SYNOV4008440, TBAES2001229,
 TBAES2001258, TESOP2004114, TESOP2005485, TESOP2009121,
 TESTI1000257, TESTI1000319, TESTI2000644, TESTI2002618,
 5 TESTI2005610, TESTI2024567, TESTI2026505, TESTI2050987,
 TESTI2051867, TESTI2053399, TESTI2053621, TESTI4000014,
 TESTI4000079, TESTI4000288, TESTI4000349, TESTI4000724,
 TESTI4001148, TESTI4001176, TESTI4001527, TESTI4001561,
 TESTI4002491, TESTI4006420, TESTI4006819, TESTI4007163,
 10 TESTI4007778, TESTI4007810, TESTI4008050, TESTI4008429,
 TESTI4009160, TESTI4009457, TESTI4009881, TESTI4010851,
 TESTI4011745, TESTI4011956, TESTI4012406, TESTI4012448,
 TESTI4012505, TESTI4012679, TESTI4013369, TESTI4013924,
 TESTI4014175, TESTI4016110, TESTI4016822, TESTI4016925,
 15 TESTI4017901, TESTI4018835, TESTI4018881, TESTI4018886,
 TESTI4020092, TESTI4021478, TESTI4022873, TESTI4023546,
 TESTI4026524, TESTI4027557, TESTI4028059, TESTI4028429,
 TESTI4028880, TESTI4030069, TESTI4034632, TESTI4034912,
 TESTI4035063, TESTI4035498, TESTI4036909, TESTI4037156,
 20 TESTI4040363, THYMU1000496, THYMU2005303, THYMU2008725,
 THYMU2019210, THYMU2027497, THYMU2027695, THYMU2027734,
 THYMU2031046, THYMU2033104, THYMU2035319, THYMU2037233,
 THYMU2041015, THYMU3001083, THYMU3001234, THYMU3001379,
 THYMU3003309, THYMU3004835, THYMU3006118, THYMU3007137,
 25 THYMU3008436, TKIDN2000701, TKIDN2006852, TLIVE2001327,
 TRACH2001549, TRACH2007059, TRACH2022425, TRACH2022649,
 TRACH3000558, TRACH3002168, TRACH3004721, TRACH3004786,
 TRACH3005549, TRACH3007479, TRACH3008629, TRACH3009455,
 TRACH3035526, TSTOM2000442, TUTER2000904, UTERU1000337,
 30 UTERU2005621, UTERU2007724, UTERU2017762, UTERU2019491,
 UTERU2019706, UTERU2025025, UTERU2026090, UTERU2027591,
 UTERU2035328, UTERU3000645, UTERU3000828, UTERU3000899,
 UTERU3001240, UTERU3001572, UTERU3001585, UTERU3001652,
 UTERU3003116, UTERU3003135, UTERU3005907, UTERU3007640,
 35 UTERU3008671, UTERU3009490, UTERU3009690, UTERU3009979,
 UTERU3015500, UTERU3016789

The following 84 clones are also predicted to belong to the category of disease-related protein.

BRACE3001113, BRACE3010076, BRAMY2039341, BRAMY3004800,
 BRAWH3009017, BRCAN2002473, BRCAN2002854, BRCAN2003070,
 5 BRHIP2005271, BRHIP2017553, BRHIP2026877, BRHIP3000240,
 BRHIP3008314, BRHIP3026052, BRSTN2013354, BRTHA2016318,
 BRTHA2017972, BRTHA3003000, CERVX2002013, CTONG1000113,
 CTONG2008721, CTONG2020411, CTONG3004550, FCBBF1000509,
 FEBRA2008692, HCASM2008536, HCHON2004858, HEART2009680,
 10 HLUNG2015548, HSYRA2005628, IMR322008651, IMR322013396,
 MESAN2001770, NT2RI2009583, NT2RI3007443, OCBBF2003327,
 OCBBF2009583, OCBBF2011669, OCBBF2024284, OCBBF2032274,
 OCBBF3000167, OCBBF3002654, PLACE7000502, PROST2000452,
 PROST2009320, SPLEN2004611, STOMA2003158, SYNOV1000256,
 15 SYNOV4002744, SYNOV4003981, TBAES2000932, TESOP2000390,
 TESOP2001796, TESOP2005199, TESTI2015626, TESTI2025924,
 TESTI2026647, TESTI2039060, TESTI4000183, TESTI4006473,
 TESTI4011070, TESTI4017714, TESTI4019657, TESTI4021482,
 TESTI4024387, TESTI4025494, TESTI4025547, TESTI4028938,
 20 TESTI4031745, TESTI4032112, THYMU2004284, THYMU2028739,
 THYMU2031139, THYMU2031249, THYMU2035710, THYMU3000269,
 TLIVE2001684, TLIVE2002046, TRACH2024408, TRACH3003683,
 UTERU2021820, UTERU2032279, UTERU2033577, UTERU3000738

In particular, hit data of the following 338 clones for
 25 Swiss-Prot, or GenBank, UniGene, nr or RefSeq corresponded to
 genes or proteins which had been deposited in the Online
 Mendelian Inheritance in Man (OMIM), which is the human gene and
 disease database (the OMIM Number is shown in the parenthesis
 after the Clone Name).

30 3NB692002806 (261630), ADIPS2000088 (147120), BLADE2005036
 (114850), BRACE2005457 (274600;603545;600791), BRACE2008594
 (601959), BRACE2014306 (193002), BRACE2016981 (602701),
 BRACE2018762 (604800), BRACE2035381 (606088), BRACE2038551
 (601961),
 35 BRACE2039249 (602273), BRACE2045300 (601442), BRACE3000840
 (600355), BRACE3001002 (300236), BRACE3001391 (601313;173900),

BRACE3001754 (185641), BRACE3002508 (606417), BRACE3003595
 (602941), BRACE3004058 (250800), BRACE3004150 (601035),
 BRACE3004772 (603143), BRACE3008137 (602187), BRACE3008384
 (603264), BRACE3009708 (182340), BRACE3010397 (602187),
 5 BRACE3011271 (602187), BRACE3011421 (602187), BRACE3014807
 (605784), BRACE3015027 (602187), BRACE3015521 (605888),
 BRACE3018963 (605744), BRACE3020594 (400023), BRACE3027326
 (602187), BRALZ2017359 (604331), BRAMY2005052 (602621),
 BRAMY2038904 (605671), BRAMY2047751 (602512), BRAMY3000213
 10 (605448), BRAMY3005091 (600286), BRAMY3007609 (300315),
 BRAMY4000095 (602187), BRAMY4000229 (602159), BRAMY4000277
 (602187), BRAWH2001395 (159430), BRAWH2002560 (602865),
 BRAWH2010000 (602581), BRAWH2010536 (604010), BRAWH2014414
 (603006), BRAWH3000100 (601403), BRAWH3000491 (602187),
 15 BRAWH3001326 (602187), BRAWH3002574 (602187), BRAWH3005912
 (602187), BRAWH3008341 (602187), BRCAN2002562 (602187),
 BRCAN2002856 (602712), BRCAN2002948 (603534), BRCAN2003746
 (311870), BRCAN2006063 (603196;601369), BRCAN2009203 (603143),
 BRCAN2014602 (601441), BRCAN2016619 (602187), BRCAN2017442
 20 (604455), BRCAN2024451 (602513), BRCOC2001505 (159430),
 BRCOC2003213 (602187), BRHIP2000819 (605000), BRHIP2001805
 (603219), BRHIP2009414 (602187), BRHIP2024165 (604402),
 BRHIP2026288 (602187), BRHIP3000339 (159430), BRHIP3008405
 (602187), BRHIP3009448 (602187), BRHIP3027137 (600249),
 25 BRHIP3027854 (601060), BRSSN2000684 (603505), BRSSN2004719
 (600560), BRSSN2014424 (606105), BRSTN2001613 (164020),
 BRSTN2004987 (604733), BRSTN2008418 (602187), BRTHA2002608
 (600463), BRTHA2003110 (602187), BRTHA2007122 (106410),
 BRTHA2007603 (605846), BRTHA2008527 (152790;176410),
 30 BRTHA2012980 (300119), BRTHA2014792 (601674), BRTHA3001721
 (604902),
 BRTHA3002427 (602187), BRTHA3003074 (605367), BRTHA3003449
 (160745), BRTHA3008778 (602187), BRTHA3009037 (602187),
 BRTHA3009090 (603197), BRTHA3015815 (600902), BRTHA3016917
 35 (604137), BRTHA3017848 (603377;212140), COLON2000568 (147000),
 COLON2002520 (602187), CTONG1000341 (188040), CTONG2000042

(103950), CTONG2009423 (182137), CTONG2010803 (602189),
 CTONG2023021 (602498), CTONG2025496 (103950), CTONG2025516
 (601679), CTONG3000084 (600888), CTONG3002412 (601403),
 CTONG3008639 (601797), D3OST2002182 (603590), D3OST2002648
 5 (603071), DFNES2001108 (603560), FCBBF3009888 (602470),
 FEBRA2007708 (126650;214700), FEBRA2008468 (278000),
 HCASM2001301 (602399), HCASM2007737 (601504), HCHON2001712
 (109190),
 HCHON2002676 (252800), HCHON2003532 (172490), HCHON2004007
 10 (605866), HCHON2004531 (602187), HCHON2008112 (605837),
 HCHON2008444 (602187), HEART1000010 (602187), HEART1000139
 (191045;115195), HEART2001680 (146900), HEART2010495 (157132),
 HLUNG2002465 (605216), HSYRA2005496 (131195;187300),
 IMR322000127 (604077), IMR322001380 (605652), IMR322006495
 15 (605607), KIDNE2012945 (600270), NOVAR2001108 (147120),
 NT2NE2003252 (602913), NT2NE2006531 (602277), NT2NE2006909
 (602187),
 NT2RI2006686 (602700), NT2RI2025909 (212138), NT2RI3001515
 (300362), NT2RI3006171 (114890), NT2RI3006340 (602187),
 20 NT2RI3006673 (602187), NT2RI3007757 (605396), NT2RI3008652
 (602654), NT2RP7000359 (603271), NT2RP7005118 (603379),
 NT2RP7005529 (600888), NT2RP7010599 (603684), NTONG2000413
 (602262), OCBBF2006058 (604773), OCBBF2020801 (602187),
 OCBBF2021788 (602597), OCBBF2031167 (603709), OCBBF2033869
 25 (600270), OCBBF2036743 (604075), OCBBF2037068 (602187),
 OCBBF2037340 (602187), OCBBF3003320 (605868), PEBLM2000170
 (602187), PEBLM2002887 (602187), PERIC2003720 (600381),
 PERIC2007914 (400009), PERIC2008385 (604455), PERIC2009086
 (600134;605158), PLACE5000282 (130160), PLACE6019385 (602448),
 30 PROST1000184 (192321), PROST2003428 (602187), PROST2016462
 (602187), PROST2017367 (600585), PROST2018090 (312610),
 PROST2018511 (602187), PUAEN2002489 (604658), PUAEN2009795
 (601456), SKNMC2007504 (602187), SMINT2010076 (146900),
 SPLEN2002467 (605652), SPLEN2006122 (604739), SPLEN2011422
 35 (114213), SPLEN2012624 (602187), SPLEN2021701 (142800),
 SPLEN2031547 (602187), SPLEN2033098 (602746), SPLEN2036326

(602101), SPLEN2036821 (212138), SPLEN2036932 (605577),
 SYNOV2005817 (123889), SYNOV2012326 (604336), SYNOV2014400
 (135820), SYNOV2021320 (602104), SYNOV3000231 (147100),
 SYNOV3000302 (147100), SYNOV4002883 (602187), SYNOV4004741
 5 (602187), SYNOV4007360 (602187), SYNOV4007521 (605830),
 SYNOV4007553 (603028), SYNOV4007671 (602187), SYNOV4008440
 (602187), TBAES2001229 (602187), TBAES2001258 (142440),
 TESOP2004114 (601865), TESOP2005485 (147170), TESOP2009121
 (117143), TESTI1000257 (138170), TESTI1000319 (602187),
 10 TESTI2000644 (601392), TESTI2002618 (601533), TESTI2005610
 (601040), TESTI2024567 (601116), TESTI2026505 (305400),
 TESTI2050987 (605968), TESTI2051867 (180479), TESTI2053399
 (605819), TESTI2053621 (600364;602093), TESTI4000014 (602187),
 TESTI4000079 (603560), TESTI4000288 (602187), TESTI4000349
 15 (604506), TESTI4000724 (603878), TESTI4001148 (602187),
 TESTI4001176 (601430), TESTI4001527 (602187), TESTI4001561
 (602187), TESTI4002491 (602187), TESTI4006420 (605612),
 TESTI4006819 (602187), TESTI4007163 (602187), TESTI4007778
 (602187), TESTI4007810 (600940), TESTI4008050 (602187),
 20 TESTI4008429 (602187), TESTI4009160 (602187), TESTI4009457
 (606185), TESTI4009881 (602187), TESTI4010851 (602187),
 TESTI4011745 (602187), TESTI4011956 (602187), TESTI4012406
 (602187), TESTI4012448 (185261), TESTI4012505 (602143),
 TESTI4012679 (601933), TESTI4013369 (602187), TESTI4013924
 25 (602187), TESTI4014175 (602187), TESTI4016110 (602187),
 TESTI4016822 (601792), TESTI4016925 (602187), TESTI4017901
 (104221), TESTI4018835 (602187), TESTI4018881 (605070),
 TESTI4018886 (602187), TESTI4020092 (156225), TESTI4021478
 (605868), TESTI4022873 (602187), TESTI4023546 (602187),
 30 TESTI4026524 (603277), TESTI4027557 (602187), TESTI4028059
 (232800;171850), TESTI4028429 (602187), TESTI4028880 (138170),
 TESTI4030069 (604603), TESTI4034632 (606251), TESTI4034912
 (602187), TESTI4035063 (602187), TESTI4035498 (602187),
 TESTI4036909 (602187), TESTI4037156 (606026), TESTI4040363
 35 (185641), THYMU1000496 (603060), THYMU2005303 (186910),
 THYMU2008725 (176882), THYMU2019210 (142830), THYMU2027497

(182139), THYMU2027695 (147100), THYMU2027734 (145505),
 THYMU2031046 (604207), THYMU2033104 (605349), THYMU2035319
 (604739), THYMU2037233 (605121), THYMU2041015 (602187),
 THYMU3001083 (602187), THYMU3001234 (602187), THYMU3001379
 5 (602187), THYMU3003309 (300359), THYMU3004835 (602187),
 THYMU3006118 (603708), THYMU3007137 (602187), THYMU3008436
 (602187), TKIDN2000701 (600465), TKIDN2006852 (603602),
 TLIVE2001327 (601403), TRACH2001549 (603197), TRACH2007059
 (602187), TRACH2022425 (146900), TRACH2022649 (147100),
 10 TRACH3000558 (600140), TRACH3002168 (155735), TRACH3004721
 (602187), TRACH3004786 (602187), TRACH3005549 (602187),
 TRACH3007479 (602308), TRACH3008629 (600976), TRACH3009455
 (171833), TRACH3035526 (147000), TSTOM2000442 (147100),
 TUTER2000904 (602187), UTERU1000337 (602187), UTERU2005621
 15 (603505), UTERU2007724 (602373), UTERU2017762 (601053),
 UTERU2019491 (603762), UTERU2019706 (600114), UTERU2025025
 (191315;164970;256000), UTERU2026090 (605497), UTERU2027591
 (600150),
 UTERU2035328 (605409), UTERU3000645 (602909), UTERU3000828
 20 (602187), UTERU3000899 (603062), UTERU3001240 (602187),
 UTERU3001572 (602187), UTERU3001585 (602187), UTERU3001652
 (602715), UTERU3003116 (602187), UTERU3003135 (602187),
 UTERU3005907 (190196), UTERU3007640 (603215), UTERU3008671
 (182120), UTERU3009490 (604585), UTERU3009690 (104221),
 25 UTERU3009979 (600441), UTERU3015500 (606667), UTERU3016789
 (602104)

Additionally, hit data of the following 84 clones for
 Swiss-Prot, nr or RefSeq corresponded to genes or proteins which
 had been deposited in the Online Mendelian Inheritance in Man
 30 (OMIM), which is the human gene and disease database (the OMIM
 Number is shown in the parenthesis after the Clone Name).
 BRACE3001113 (603971), BRACE3010076 (142695), BRAMY2039341
 (604077), BRAMY3004800 (602187), BRAWH3009017 (602187),
 BRCAN2002473 (602187), BRCAN2002854 (602895), BRCAN2003070
 35 (605574), BRHIP2005271 (600267), BRHIP2017553 (602187),
 BRHIP2026877 (600341), BRHIP3000240 (601142), BRHIP3008314

(604480), BRHIP3026052 (601645), BRSTN2013354 (602187),
 BRTHA2016318 (605442), BRTHA2017972 (602932), BRTHA3003000
 (605276), CERVX2002013 (602903), CTONG1000113 (602277),
 CTONG2008721 (605317), CTONG2020411 (601930), CTONG3004550
 5 (605611), FCBBF1000509 (601933), FEBRA2008692 (604034),
 HCASM2008536 (194360), HCHON2004858 (602187), HEART2009680
 (601970), HLUNG2015548 (146690), HSYRA2005628 (602187),
 IMR322008651 (179617), IMR322013396 (600053), MESAN2001770
 (600495), NT2RI2009583 (605949), NT2RI3007443 (602448),
 10 OCBBF2003327 (605008), OCBBF2009583 (602277), OCBBF2011669
 (602187), OCBBF2024284 (176981), OCBBF2032274 (603975),
 OCBBF3000167 (194558), OCBBF3002654 (601893), PLACE7000502
 (164951), PROST2000452 (602060), PROST2009320 (605903),
 SPLEN2004611 (602228), STOMA2003158 (602244), SYNOV1000256
 15 (606021), SYNOV4002744 (602187), SYNOV4003981 (604283),
 TBAES2000932 (606212), TESOP2000390 (602187), TESOP2001796
 (602187), TESOP2005199 (194531), TESTI2015626 (601249),
 TESTI2025924 (600863), TESTI2026647 (601235), TESTI2039060
 (154360), TESTI4000183 (601276), TESTI4006473 (602187),
 20 TESTI4011070 (602187), TESTI4017714 (602187), TESTI4019657
 (602052), TESTI4021482 (164730), TESTI4024387 (602187),
 TESTI4025494 (602187), TESTI4025547 (605308), TESTI4028938
 (603899), TESTI4031745 (602448), TESTI4032112 (603246),
 THYMU2004284 (314370), THYMU2028739 (604191), THYMU2031139
 25 (605009), THYMU2031249 (311550), THYMU2035710 (601890),
 THYMU3000269 (600857), TLIVE2001684 (120700), TLIVE2002046
 (125270), TRACH2024408 (106410), TRACH3003683 (150205),
 UTERU2021820 (126141), UTERU2032279 (600942), UTERU2033577
 (603397), UTERU3000738 (602187)

30 The clones predicted to belong to the category of enzyme
 and/or metabolism-related protein are the following 171 clones.
 3NB692002806, ASTRO2002842, BLADE2005036, BRACE2008594,
 BRACE2030341, BRACE2035381, BRACE2038551, BRACE2039249,
 BRACE2041200, BRACE2045772, BRACE3004058, BRACE3009708,
 35 BRACE3011421, BRACE3016884, BRACE3024073, BRACE3025630,
 BRAMY2033267, BRAMY2039872, BRAMY3002803, BRAMY3004919,

BRAMY3005091, BRAMY3005932, BRAMY4000095, BRAWH3002574,
 BRAWH3008341, BRCAN2003703, BRCAN2003746, BRCAN2009432,
 BRCAN2014602, BRCAN2017442, BRCAN2028355, BRCOC2003213,
 BRHIP2024165, BRHIP3008405, BRHIP3027137, BRHIP3027854,
 5 BRSTN2000872, BRSTN2004863, BRSTN2004987, BRSTN2008418,
 BRTHA2002608, BRTHA2009311, BRTHA2015406, BRTHA2016496,
 BRTHA3008778, BRTHA3009090, BRTHA3015815, BRTHA3016917,
 CTONG2004062, CTONG2006798, CTONG2013178, CTONG2028124,
 CTONG3009028, D3OST2002182, DFNES2001108, DFNES2005266,
 10 FCBBF3013307, FCBBF3023895, FEBRA2008468, FEBRA2026984,
 HCASM2001301, HCHON2002676, HCHON2003532, HCHON2004007,
 HEART2006131, HEART2010492, HHDPC1000118, HLUNG2011298,
 HLUNG2013204, HSYRA2008714, KIDNE2001361, KIDNE2006580,
 NT2NE2003252, NT2NE2006909, NT2RI2004618, NT2RI2025909,
 15 NT2RI3006673, NT2RI3007978, NT2RI3008974, NT2RP7000359,
 NT2RP7004027, NT2RP7010599, NT2RP7014005, NTONG2000413,
 NTONG2008672, OCBBF2006005, OCBBF2006058, OCBBF2006151,
 OCBBF2019823, OCBBF2025527, OCBBF2030354, OCBBF2031167,
 OCBBF3003320, PEBLM2005183, PERIC2000889, PERIC2008385,
 20 PLACE6019385, PLACE7008431, PROST2017367, PUAEN2007044,
 PUAEN2009655, PUAEN2009852, SKNMC2006998, SKNMC2007504,
 SMINT1000192, SPLEN2010912, SYNOV2012326, SYNOV4002883,
 TBAES2001258, TESOP2000801, TESOP2004114, TESTI2005610,
 TESTI2005739, TESTI2016046, TESTI4000079, TESTI4000209,
 25 TESTI4000288, TESTI4000349, TESTI4001176, TESTI4001527,
 TESTI4001561, TESTI4002552, TESTI4006148, TESTI4006819,
 TESTI4007810, TESTI4008429, TESTI4010851, TESTI4012406,
 TESTI4012448, TESTI4013369, TESTI4013817, TESTI4014175,
 TESTI4016822, TESTI4018152, TESTI4018835, TESTI4019566,
 30 TESTI4021478, TESTI4022716, TESTI4023546, TESTI4026510,
 TESTI4026524, TESTI4028059, TESTI4029836, TESTI4034632,
 TESTI4036909, TESTI4046819, THYMU2008725, THYMU2027734,
 THYMU2031046, THYMU2031258, THYMU3001234, THYMU3003212,
 THYMU3004157, THYMU3004835, THYMU3006118, THYMU3008436,
 35 TKIDN2006852, TLIVE2002336, TRACH2001549, TRACH2009310,
 TRACH3007479, TRACH3036193, UTERU1000337, UTERU2019491,

UTERU2025025, UTERU2026203, UTERU3000665, UTERU3001240,
UTERU3001585, UTERU3003116, UTERU3005907

The following 59 clones are also predicted to belong to the category of enzyme and/or metabolism-related protein.

5 BRACE2039823, BRACE3010076, BRAMY2038516, BRAWH1000369,
BRCAN2003070, BRHIP2005271, BRHIP2012360, BRHIP2026877,
BRHIP3008314, BRTHA2013610, BRTHA2017364, BRTHA2017972,
BRTHA2018011, BRTHA2018443, BRTHA3003000, CTONG2016942,
FCBBF1000509, FEBRA2008692, HCASM2003099, HLUNG2015548,
10 MESAN2005303, NT2RI3000174, NT2RI3007443, NT2RP7008435,
NTONG2008093, OCBBF2003327, OCBBF2034637, OCBBF3002654,
PROST2000452, SPLEN2039311, SPLEN2039379, STOMA2003158,
TESOP2000390, TESTI2015626, TESTI2025924, TESTI2026647,
TESTI2032643, TESTI2036288, TESTI2039060, TESTI4006473,
15 TESTI4011070, TESTI4014801, TESTI4017714, TESTI4019657,
TESTI4021482, TESTI4031745, THYMU2004139, THYMU2004284,
THYMU2031139, THYMU2031249, THYMU2040925, THYMU3000269,
TLIVE2002046, TLIVE2007607, TRACH2024559, TRACH3003683,
TRACH3007866, UTERU2021820, UTERU3000738

20 The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 42 clones.

BLADE2002782, BRACE2042550, BRACE2043248, BRACE3000840,
BRALZ2017359, BRAMY2038484, BRAMY2046989, BRAWH2010536,
25 BRAWH2014954, BRAWH3000100, BRHIP2000819, BRHIP2001927,
BRHIP2009414, BRSSN2000684, CTONG3002412, CTONG3008258,
CTONG3008639, FCBBF3002163, HCASM2001301, IMR322006495,
NT2RI2006686, OCBBF2021020, OCBBF2037068, OCBBF3004314,
PLACE5000282, PLACE6019385, PLACE7002641, PUAEN2006328,
30 SPLEN2033098, TESOP2009121, TESTI1000545, TESTI2003573,
TESTI2005610, TESTI4007810, TESTI4017901, THYMU2034374,
THYMU2039315, TLIVE2001327, TRACH2025507, UTERU2005621,
UTERU3009690, UTERU3009979

35 The following ten clones are also predicted to belong to the category of cell division and/or cell proliferation-related protein.

BRCAN2003070, BRTHA3003000, NT2RI3007443, PLACE7000502,
 SPLEN2004611, STOMA2003158, SYNOV4003981, TESTI4031745,
 THYMU2004139, THYMU2035078

5 The clones predicted to belong to the category of
 cytoskeleton-related protein are the following 55 clones.

ASTRO1000009, BLADE2004089, BRACE2026836, BRACE2045300,
 BRACE3006872, BRAMY3008466, BRAWH2001395, BRAWH2005315,
 BRAWH3002600, BRCOC2001505, BRHIP2000819, BRHIP3000339,
 BRHIP3008405, BRTHA2007122, BRTHA3003449, COLON2002520,
 10 CORDB2000541, FCBBF3021940, HCHON2001577, HEART1000139,
 HEART2010495, NT2RI3006340, NT2RP7000359, NTONG2005277,
 OCBBF2007068, OCBBF3003592, PERIC2000889, PLACE5000282,
 PROST1000559, SKMUS2006394, SPLEN2011422, SPLEN2015679,
 TESTI2049857, TESTI4000288, TESTI4001148, TESTI4007778,
 15 TESTI4009160, TESTI4009881, TESTI4011956, TESTI4013924,
 TESTI4016925, TESTI4018886, TESTI4022873, TESTI4034912,
 TESTI4035063, TESTI4037727, THYMU1000496, THYMU2035735,
 THYMU3001083, THYMU3001234, TKIDN2000701, UTERU2007724,
 UTERU2008347, UTERU2035745, UTERU3003178

20 The following six clones are also predicted to belong to
 the category of cytoskeleton-related protein.

HLUNG2015418, SPLEN2030847, SPLEN2036702, TESTI4025268,
 TESTI4026207, TRACH2024408

25 The clones predicted to belong to the category of nuclear
 protein and/or RNA synthesis-related protein are the following
 42 clones.

BLADE2007958, BRACE2010489, BRACE2045300, BRACE3004150,
 BRACE3005430, BRACE3011421, BRAMY2046989, BRAMY3005932,
 BRCAN2002562, BRHIP2021615, BRSTN2001613, BRSTN2004987,
 30 COLON2000470, CTONG3009028, FCBBF3013307, HCHON2004531,
 IMR322006495, OCBBF2020801, PEBLM2005183, PUAEN2007044,
 SKNMC1000124, SMINT1000192, SPLEN2006122, SPLEN2010912,
 TESOP2009121, TESTI4009374, TESTI4009457, TESTI4013830,
 TESTI4019566, TESTI4022716, THYMU2033104, THYMU2035319,
 35 THYMU2038301, THYMU2040975, THYMU3001379, TRACH3004721,

TRACH3036609, UTERU2026025, UTERU3000828, UTERU3001572,
UTERU3003135, UTERU3004992

The following 16 clones are also predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein.

5 BRACE3010076, BRCAN2002854, BRHIP2006617, BRHIP2012360,
BRHIP3026052, BRSTN2013354, BRTHA2017364, HCASM2003099,
HCASM2008536, IMR322008651, NT2RI3000174, STOMA2003158,
TESTI2026647, TESTI4006473, TESTI4021482, THYMU2035078

10 The clones predicted to belong to the category of protein
synthesis and/or transport-related protein are the following 57
clones.

ASTRO2002842, BLADE2005036, BRACE3025630, BRAMY2033003,
BRAMY3007609, BRAWH3000491, BRAWH3002574, BRAWH3008341,
BRCAN2002856, BRCAN2002948, BRCOC2003213, BRSTN2004987,
15 BRTHA2016496, BRTHA3013884, BRTHA3016917, CTONG2000042,
CTONG2013178, CTONG2023512, CTONG2024749, CTONG2025496,
CTONG3001370, DFNES2005266, FEBRA2026984, HCASM2007737,
HCHON2008444, HEART1000010, KIDNE2000846, NT2NE2006909,
NT2RI2011422, NT2RP7004027, NTONG2000413, OCBBF2031167,
20 TBAES2001229, TBAES2001258, TESTI1000319, TESTI2005610,
TESTI2051867, TESTI4000209, TESTI4000349, TESTI4001106,
TESTI4002491, TESTI4008050, TESTI4010851, TESTI4012406,
TESTI4012448, TESTI4013924, TESTI4028429, TESTI4034912,
THYMU2009157, TLIVE2008229, TRACH3007479, TRACH3008713,
25 TRACH3036193, UTERU2019940, UTERU3001988, UTERU3003116,
UTERU3007419

The following 15 clones are also predicted to belong to the category of protein synthesis and/or transport-related protein.

BRTHA2007060, BRTHA2018011, CTONG2016942, MESAN2001770,
30 MESAN2005303, NT2RP7008435, OCBBF2003327, PROST2000452,
TESOP2001796, TESTI4017714, THYMU2004284, THYMU2031139,
TRACH2024559, TRACH3007866, UTERU2021820

The clones predicted to belong to the category of cellular defense-related protein are the following three clones.

35 BRACE3005430, HCHON2004531, TESTI4007810

The following four clones are also predicted to belong to the category of cellular defense-related protein.

BRHIP2012360, FCBBF3027854, HCASM2008536, UTERU2032279

5 The clones predicted to belong to the category of development and/or differentiation-related protein are the following nine clones.

BRACE3009747, BRTHA2005579, BRTHA3003343, IMR322000917,
PEBLM2000170, TESOP2001122, TESOP2001953, TESTI2040018,
UTERU3006308

10 The following five clones are also predicted to belong to the category of development and/or differentiation-related protein.

BRALZ2017844, CTONG2020378, HCHON2004858, OCBBF2019684,
THYMU2006001

15 The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 55 clones.

3NB692002685, BLADE2007958, BRACE2030326, BRACE2045596,
BRACE3001002, BRACE3004150, BRACE3009747, BRACE3045033,
BRCAN2002562, BRHIP2021615, BRSSN2014299, BRSTN2001613,
20 BRSTN2004987, BRTHA2014792, BRTHA3001721, BRTHA3003343,
CTONG2025516, CTONG3008831, CTONG3009028, FCBBF3013307,
FEBRA2007544, FEBRA2007801, HEART1000074, IMR322000127,
IMR322000917, NT2NE2006531, NT2RI3009158, OCBBF2020838,
OCBBF2036743, PEBLM2002887, PEBLM2005183, SKNMC2007504,
25 SMINT1000192, SPLEN2006122, TBAES2001229, TESTI2014716,
TESTI2040018, TESTI2044796, TESTI4009374, TESTI4012679,
TESTI4014175, TESTI4017543, TESTI4026510, TESTI4026524,
THYMU2006420, THYMU2035319, THYMU2037233, THYMU2040975,
THYMU3004866, TLIVE2008229, TRACH3036609, TUTER2000425,
30 UTERU2026025, UTERU2035328, UTERU3009490

The following 74 clones are also predicted to belong to the category of DNA-binding and/or RNA-binding protein.

BRACE2003609, BRACE3001058, BRACE3001113, BRACE3010076,
BRALZ2017844, BRAMY2035070, BRAMY2035449, BRAMY2035718,
35 BRAMY2039341, BRAWH1000369, BRAWH2006207, BRCAN2002854,
BRHIP2012360, BRHIP2017553, BRSTN2013354, BRTHA2017364,

CERVX2002013, CTONG1000113, CTONG2008721, CTONG2020378,
 CTONG2020411, CTONG2028758, CTONG3004726, DFNES2011192,
 FEBRA2014122, FEBRA2027609, HCASM2003018, HCASM2009424,
 HCHON2004858, HSYRA2005628, IMR322008651, MESAN2001770,
 5 MESAN2005303, MESAN2014412, MESAN2015501, NT2RI2008952,
 NT2RI2018448, NT2RI3000174, NT2RI3001132, OCBBF2008144,
 OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2032274,
 OCBBF3000167, SPLEN2004611, SPLEN2016135, SPLEN2016781,
 SYNOV2021953, SYNOV4002744, TESOP2005199, TESOP2006398,
 10 TESOP2006865, TESTI2026647, TESTI2034251, TESTI4000183,
 TESTI4000214, TESTI4006473, TESTI4008302, TESTI4015442,
 TESTI4025494, TESTI4025547, TESTI4028938, TESTI4032112,
 THYMU2006001, THYMU2035078, TRACH2007483, TRACH3000134,
 TRACH3002561, TRACH3003832, TUTER2000057, UTERU2033577,
 15 UTERU3001053, TESTI4038779

The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 68 clones.

BNGH42007788, BRACE2008594, BRACE2047377, BRACE3005430,
 BRACE3008720, BRACE3009708, BRACE3015521, BRACE3024073,
 20 BRAMY4000095, BRCAN2009432, BRCOC2003213, BRHIP3008405,
 BRSTN2013741, BRTHA3003449, BRTHA3015815, BRTHA3016917,
 COLON2002520, FEBRA2026984, HCASM2001301, HCHON2004007,
 HSYRA2008714, KIDNE2001361, KIDNE2001847, NESOP2001694,
 NT2RI2005166, NT2RP7013795, OCBBF3003320, OCBBF3003592,
 25 PEBLM2002594, PERIC2000889, PLACE6019385, SMINT1000192,
 SPLEN2037194, TESOP2000801, TESTI2006648, TESTI4000288,
 TESTI4001148, TESTI4001176, TESTI4002552, TESTI4007810,
 TESTI4008429, TESTI4009160, TESTI4009881, TESTI4011956,
 TESTI4013817, TESTI4014175, TESTI4016925, TESTI4018208,
 30 TESTI4018835, TESTI4019566, TESTI4021478, TESTI4022873,
 TESTI4026524, TESTI4029836, TESTI4035498, TESTI4036909,
 TESTI4037727, THYMU1000496, THYMU2033079, THYMU3001083,
 THYMU3001234, THYMU3001379, TRACH2009310, UTERU2019706,
 UTERU2025025, UTERU2035745, UTERU3000665, UTERU3000828

35 The following 24 clones are also predicted to belong to the category of ATP binding and/or GTP-binding protein.

BRHIP2026877, BRTHA2017364, BRTHA2018443, IMR322008651,
 IMR322013731, NT2RI3007443, NTONG2008093, OCBBF3002654,
 TESOP2000390, TESOP2007384, TESTI2025924, TESTI2026647,
 TESTI2049956, TESTI4005317, TESTI4006473, TESTI4021482,
 5 TESTI4026207, TESTI4031745, THYMU2004139, THYMU2031249,
 TRACH2000862, TRACH2024559, TRACH3000420, UTERU3000738

The 119 clones shown below are clones which were
 unassignable to any of the above-mentioned categories, but have
 been predicted to have some function based on homology search
 10 using their full-length nucleotide sequences. Clone Name and
 Definition in the result of homology search, demarcated by a
 double slash mark (//), are shown below.

ADRGL2009691// Mus musculus D11lgp1 mRNA, complete cds.
 ADRGL2009755// Homo sapiens brain and reproductive organ-
 15 expressed protein (BRE) mRNA, complete cds.
 ASTRO3000177// Drosophila melanogaster BcDNA.GH03694
 (BcDNA.GH03694) mRNA, complete cds.
 BLADE2008398// Homo sapiens LRR FLI-I interacting protein 2
 (LRRFIP2) mRNA, complete cds.
 20 BRACE2006319// Homo sapiens mRNA for Fln29, complete cds.
 BRACE2027258// Homo sapiens E2a-Pbx1-associated protein (EB-1)
 mRNA, partial cds.
 BRACE2038329// Rattus norvegicus CBL-B (Cbl-b) mRNA, partial cds.
 BRACE2046251// Homo sapiens hucep-10 mRNA for cerebral protein-
 25 10, complete cds.
 BRACE3003192// latent transforming growth factor beta binding
 protein 3 [Homo sapiens]
 BRACE3007625// espin [Rattus norvegicus]
 BRACE3009297// mdgl-1 [Mus musculus]
 30 BRACE3015262// espin [Mus musculus]
 BRACE3025457// testis-specific protein TSP-NY [Homo sapiens]
 BRALZ2016498// Homo sapiens FKSG76 (FKSG76) mRNA, complete cds.
 BRAMY2030109// Homo sapiens hucep-4 mRNA for cerebral protein-4,
 complete cds.
 35 BRAMY2031317// Mus musculus semaphorin cytoplasmic domain-
 associated protein 3A (Semcap3) mRNA, complete cds.

- BRAMY2047746// nasopharyngeal carcinoma susceptibility protein
[Homo sapiens]
- BRAMY3001794// Rattus norvegicus Circadian Oscillatory Protein
(SCOP) (Scop)
- 5 BRAWH2001940// H.sapiens gene from PAC 1026E2, partial.
BRAWH2012162// KE03 protein [Homo sapiens]
BRAWH2016724// MAP2=HMW-MAP2 {alternatively spliced} [rats,
brain, mRNA Partial, 267 nt].
BRAWH3002821// synaptotagmin-like 2 [Mus musculus]
- 10 BRCAN2002944// Mus musculus huntington yeast partner C (Hypc)
mRNA, complete cds.
BRCAN2013660// Arabidopsis thaliana putative protein (F4F15.330)
mRNA, complete cds.
BRHIP2002122// Homo sapiens B aggressive lymphoma long isoform
15 (BAL) mRNA, complete cds.
BRHIP2003786// CCA3 [Rattus norvegicus]
BRHIP2004359// ELAC PROTEIN.
BRHIP2007616// plexin 2
BRHIP2029393// COBW-like protein [Homo sapiens]
- 20 BRHIP3008313// testis specific ankyrin-like protein 1 [Homo
sapiens]
BRSSN2013874// TEMO [Rattus norvegicus]
BRSTN2017771// Homo sapiens putative BTK-binding protein mRNA,
complete cds.
- 25 BRTHA2012392// Homo sapiens HCDI (HCDI) mRNA, complete cds.
BRTHA3002933// uroplakin 3 [Homo sapiens]
BRTHA3008310// Mus musculus mRNA for iroquois homeobox protein 6
(Irx6 gene).
BRTHA3008520// sporulation-induced transcript 4-associated
30 protein; hypothetical protein FLJ11058 [Homo sapiens]
COLON2001721// GLUT4 vesicle protein [Mus musculus]
CTONG1000467// Mus musculus mRNA for Deltex3, complete cds.
CTONG2020026// Drosophila melanogaster BcDNA.GH09358
(BcDNA.GH09358) mRNA, complete cds.
- 35 CTONG3001123// Mus musculus Pax transcription activation domain
interacting protein PTIP mRNA, complete cds.

CTONG3002127// granuphilin [Mus musculus]
 CTONG3004072// GL002 protein [Homo sapiens]
 CTONG3006186// syntaxin binding protein 4 [Mus musculus]
 CTONG3008894// Mus musculus SH3-domain binding protein 5
 5 FCBBF1000297// Human protein immuno-reactive with anti-PTH
 polyclonal antibodies mRNA, partial cds.
 HCHON2000028// Homo sapiens 7h3 protein mRNA, partial cds.
 HCHON2000626// X-linked protein STS1769.
 HCHON2001217// Homo sapiens cullin CUL4B (CUL4B) mRNA, complete
 10 cds.
 HEART2006909// Hemolysin C.
 HLUNG2011041// basic proline-rich peptide IB-8a - human
 (fragments)
 HLUNG2014288// Mus musculus RP42 mRNA, complete cds.
 15 IMR322006886// Homo sapiens hepatocellular carcinoma-associated
 antigen 127 (HCA127) mRNA, complete cds.
 KIDNE2002252// Drosophila melanogaster BcDNA.GH09358
 (BcDNA.GH09358) mRNA, complete cds.
 KIDNE2011532// similar to melanoma-associated chondroitin
 20 sulfate proteoglycan 4
 NT2RI2012990// 76.5 KDA PROTEIN C21ORF13.
 NT2RI2025957// LU1 protein [Homo sapiens]
 NT2RI3006284// Homo sapiens chorea-acanthocytosis (CHAC) mRNA,
 complete cds.
 25 NT2RI3008697// erythroblast macrophage protein [Mus musculus]
 NT2RP8000296// similar to Kelch proteins
 NTONG2007517// RING CANAL PROTEIN (KELCH PROTEIN).
 OCBBF2002124// p40 [Homo sapiens]
 OCBBF2007610// PSD-95/SAP90-associated protein-4 [Rattus
 30 norvegicus].
 OCBBF2021323// Mus musculus GTRGEO22 (Gtrgeo22) mRNA, complete
 cds.
 OCBBF2028173// JM11 protein [Homo sapiens]
 PEBLM2001465// dipthamide biosynthesis; Dph5p [Saccharomyces
 35 cerevisiae]

- PERIC2004028// *Mus musculus* erythroblast macrophage protein EMP mRNA, complete cds.
- PLACE7006051// cytoplasmic dynein heavy chain 2 [*Rattus norvegicus*]
- 5 PROST2008993// *Mus musculus* Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
- PUAEN2003079// nasopharyngeal carcinoma susceptibility protein [*Homo sapiens*]
- SPLEN2002147// *Halocynthia roretzi* mRNA for HrPET-3, complete
- 10 cds.
- SPLEN2032154// NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43).
- SYNOV2005216// *Homo sapiens* laryngeal carcinoma related protein
- 15 1 mRNA, complete cds.
- SYNOV2007965// *Homo sapiens* mRNA for H-1(3)mbt-like protein, alternative variant a.
- SYNOV4000706// B cell phosphoinositide 3-kinase adaptor [*Mus musculus*]
- 20 TBAES2004055// NY-REN-50 antigen
- TESOP2001605// *Homo sapiens* laryngeal carcinoma related protein 1 mRNA, complete cds.
- TESOP2005285// *Homo sapiens* partial mRNA for chr2 synaptotagmin (CHR2SYT gene).
- 25 TESTI2004215// *Maackia amurensis* early nodulin (ENOD2) mRNA, partial cds.
- TESTI2009477// TRICHOHYALIN.
- TESTI2034520// *Rattus norvegicus* SMC (segregation of mitotic chromosomes 1)-like 1 (yeast) (Smc1l1), mRNA
- 30 TESTI2052693// brk kinase substrate [*Homo sapiens*].
- TESTI4006079// MUF1 protein; likely ortholog of mouse MUF1; elongin BC-interacting leucine-rich repeat protein [*Homo sapiens*]
- TESTI4006393// neural specific sr protein NSSR 2 [*Mus musculus*]
- 35 TESTI4006546// colon cancer antigen NY-CO-45 [*Homo sapiens*].

- TESTI4006802// mesothelin; megakaryocyte potentiating factor
[Mus musculus]
- TESTI4008018// DAZ associated protein 2; KIAA0058 gene product
[Homo sapiens]
- 5 TESTI4009286// Homo sapiens HOTTL protein mRNA, complete cds
TESTI4009563// testis specific ankyrin-like protein 1 [Homo
sapiens]
- TESTI4010831// yeast Sec31p homolog; ABP125 [Homo sapiens]
- TESTI4011484// Sec23-interacting protein p125 [Homo sapiens]
- 10 TESTI4014818// AD-012 protein [Homo sapiens]
- TESTI4014924// selective hybridizing clone [Mus musculus]
- TESTI4019140// Mi-2 histone deacetylase complex protein 66
[Xenopus laevis]
- TESTI4019843// Rattus norvegicus huntingtin-associated protein
15 interacting protein (duo) (Hapip), mRNA.
- TESTI4023762// Trichohyalin.
- TESTI4025920// B29 protein [Homo sapiens]
- TESTI4039659// DnaJ homolog subfamily B member 8 (mDJ6).
- TESTI4044186// leucine-rich, glioma inactivated 1 [Mus musculus]
- 20 THYMU2011736// latent transforming growth factor beta binding
protein 3
- THYMU2032825// Mus musculus mRNA for Drctnnbla, complete cds.
- THYMU2038369// Mus musculus GTRGEO22 (Gtrgeo22) mRNA, complete
cds.
- 25 THYMU3001991// ART-4 protein [Homo sapiens]
- THYMU3006172// membrane bound C2 domain containing protein
[Rattus norvegicus]
- TLIVE2003225// CUB and Sushi multiple domains 1 [Homo sapiens]
- TLIVE2004320// Homo sapiens PC2-glutamine-rich-associated
30 protein (PCQAP) mRNA, complete cds.
- TOVAR2002247// Homo sapiens partial partial mRNA for NICE-4
protein, clone 3114f17.
- TRACH2023299// growth factor receptor bound protein 2-associated
protein 2 [Mus musculus]
- 35 TRACH3000926// cardiac morphogenesis [Mus musculus]
- TRACH3001427// p47 [Homo sapiens]

TRACH3006412// Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B

TRACH3034731// Ras association (RalGDS/AF-6) domain family 2

TUTER2002729// D6MM5E protein [Mus musculus]

5 UTERU1000031// G.gallus mRNA for tom-1B protein.

UTERU2006115// ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).

UTERU2031268// NY-REN-25 antigen [Homo sapiens].

10 UTERU2035452// NG3 [Homo sapiens]

UTERU3001059// ABC1 protein homolog, mitochondrial precursor.

UTERU3005585// rhophilin-like protein [Homo sapiens]

UTERU3009871// feminization 1 homolog a (C. elegans)

The 14 clones shown below are clones which were
15 unassignable to any of the above-mentioned categories, but have been predicted to have some function based on homology search using their full-length nucleotide sequences. Clone Name and Definition in the result of homology search, demarcated by a double slash mark (//), are shown below.

20 ADRGL2000042//Homo sapiens CTCL tumor antigen se20-4 mRNA, complete cds.

BRACE3009127//oxysterol binding protein 2; oxysterol binding protein-like 1 [Homo sapiens]

BRACE3021148//DC12 protein [Homo sapiens]

25 BRAMY2040159//Homo sapiens MRIP-1 mRNA, complete cds.

BRAWH3007441//CAT56 protein [Homo sapiens]

CTONG3001501//Mus musculus glucocorticoid-induced gene 1 mRNA, complete cds.

HCHON2000508//Homo sapiens prostate antigen PARIS-1 mRNA,

30 complete cds.

OCBBF2020048// 95 kDa retinoblastoma protein binding protein; KIAA0661 gene product

PERIC2007068//Mus musculus mRNA for 1A13 protein.

TESTI4010382//cytoplasmic dynein heavy chain 2 [Rattus
35 norvegicus]

TESTI4011072//tudor domain containing 1 [Mus musculus]

TESTI4046240//sirtuin 7

UTERU2019534//Golgi apparatus protein 1 [Homo sapiens]

UTERU2028734//Mus musculus slp2-a mRNA for synaptotagmin-like protein 2-a delta 2S-III, complete cds.

Further, a polypeptide will not always belong solely to a single category of the above-described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories. Further analyses may yield additional functions for clones classified into these functional categories.

Detailed descriptions concerning each domain or motif can be found in websites linked from the websites of Pfam, InterPro (<http://www.ebi.ac.uk/interpro/>), PROSITE

(<http://www.expasy.ch/cgi-bin/prosite-list.pl>), or such. This information can be found based on domain/motif names, and accession numbers of hit data obtained through domain searches of Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) (see Example 5) for amino acid sequences deduced from the 2,495 full-length clones of the present invention whose full-length nucleotide sequences have been determined. PROSITE in

particular enables comparison of unique functional categories. The functions of polypeptides encoded by the 914 clones with hit data in Pfam were predicted and classified into the 13 functional categories described below. As a result, 661 clones were estimated to encode proteins belonging to these categories.

Secretory and/or membrane protein (87 clones)

Glycoprotein-related protein (85 clones)

Signal transduction-related protein (154 clones)

Transcription-related protein (115 clones)

Enzyme and/or metabolism-related protein (265 clones)

Cell division- and/or cell proliferation-related protein (13 clones)

Cytoskeleton-related protein (40 clones)

Nuclear protein and/or RNA synthesis-related protein (31 clones)

Protein synthesis- and/or transport-related protein (46 clones)

Cellular defense-related protein (seven clones)

Development and/or differentiation-related protein (two clones)

DNA- and/or RNA-binding protein (179 clones)

5 ATP- and/or GTP-binding protein (36 clones)

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 64 clones.

ASTRO2014923, ASTRO3000301, BRACE2005457, BRACE2014306,
BRACE3001391, BRACE3014005, BRALZ2016085, BRAMY2040592,
10 BRAWH2014662, BRHIP2004814, BRHIP3024118, BRTHA3002427,
BRTHA3017848, BRTHA3018656, CTONG2009423, CTONG2013178,
D3OST2002648, FEBRA2007708, FEBRA2008311, HCHON2001084,
HCHON2001712, HCHON2004531, HCHON2005921, HSYRA2009102,
KIDNE1000064, KIDNE2000832, NT2RI3006376, OCBBF2031167,
15 OCBBF2035110, OCBBF2038317, PEBLM2002594, PERIC1000147,
PERIC2009086, PROST1000184, SPLEN2012624, SPLEN2031547,
SPLEN2033098, SPLEN2036326, TESTI1000257, TESTI1000390,
TESTI2000644, TESTI2002036, TESTI2002928, TESTI2006648,
TESTI2024567, TESTI2034520, TESTI4000014, TESTI4000724,
20 TESTI4007163, TESTI4009881, TESTI4028880, THYMU2009425,
THYMU2011548, THYMU2033079, THYMU2041015, TLIVE2000023,
TLIVE2003381, TLIVE2007132, TRACH2006387, TRACH2007059,
TRACH3004786, UTERU3000645, UTERU3004616, UTERU3006308

25 The following 23 clones are also predicted to belong to the category of secretory protein and/or membrane protein.

BRACE2029396, BRACE3005107, BRACE3010076, BRAMY2019111,
BRAMY3004800, BRHIP3000017, FCBBF1000509, HCHON2000508,
HEART2009680, IMR322013396, NT2RI2009583, NT2RI3000174,
NT2RP8000521, OCBBF2030116, TESTI2029252, TESTI4013894,
30 TESTI4032112, TESTI4041086, THYMU2035710, TKIDN2012771,
TRACH3000420, UTERU2004299, TESTI4038779

The clones predicted to belong to the category of glycoprotein-related protein are the following 77 clones.

ADIPS2000088, BRACE2043142, BRACE2046295, BRACE3014005,
35 BRAMY2005052, BRAMY4000277, BRAWH2007658, BRCAN2006063,
BRSTN2004863, BRTHA3017589, BRTHA3017848, COLON2000568,

COLON2004478, CTONG2000042, CTONG2013178, CTONG2024206,
 CTONG2024749, CTONG2025496, CTONG3001370, CTONG3003737,
 D3OST2002182, FEBRA2007708, HCHON2001084, HCHON2002676,
 HCHON2004531, HEART2001680, HLUNG2014262, LYMPB2000083,
 5 NESOP2001433, NOVAR2001108, NT2RI3006171, NT2RI3006340,
 NT2RI3007978, NT2RP7014005, OCBBF2010140, OCBBF2037598,
 PLACE5000171, PLACE6012574, PLACE7006051, PUAEN2009174,
 SMINT2002743, SMINT2010076, SMINT2011888, SMINT2015787,
 SPLEN2001599, SPLEN2015267, SPLEN2021701, SPLEN2037722,
 10 STOMA2004294, SYNOV3000231, SYNOV3000302, SYNOV4007521,
 SYNOV4007671, TBAES2003550, TESOP2005485, TESTI2005610,
 TESTI4006326, TESTI4021294, THYMU2005303, THYMU2019210,
 THYMU2023711, THYMU2027695, TRACH2007059, TRACH2022425,
 TRACH2022553, TRACH2022649, TRACH3002168, TRACH3005479,
 15 TRACH3005549, TRACH3006470, TRACH3035526, TRACH3036609,
 TSTOM2000442, UTERU2026090, UTERU3004616, UTERU3004992,
 UTERU3006308

The following eight clones are also predicted to belong to the category of glycoprotein-related protein.

20 BRAWH2006395, BRHIP3000017, NT2RI3007443, OCBBF3002654,
 TESTI2039060, TESTI4013894, TESTI4031745, TLIVE2001684

The clones predicted to belong to the category of signal transduction-related protein are the following 116 clones.

BLADE2007958, BNGH42007788, BRACE1000258, BRACE2008594,
 25 BRACE2041009, BRACE3001391, BRACE3006872, BRACE3011421,
 BRACE3024073, BRACE3027326, BRALZ2014484, BRAMY2001473,
 BRAMY2036567, BRAMY2042760, BRAMY2047751, BRAMY3001794,
 BRAMY3002803, BRAMY3005091, BRAMY3008466, BRAMY4000095,
 BRAWH3001326, BRAWH3002821, BRAWH3005912, BRCAN2002856,
 30 BRCAN2009432, BRCAN2016619, BRCAN2024451, BRCAN2028355,
 BRHIP2000819, BRHIP2005932, BRHIP3008405, BRHIP3025161,
 BRSSN2000684, BRSSN2004719, BRSTN2008418, BRSTN2013741,
 BRTHA3009037, BRTHA3013884, COLON2001721, CTONG2006798,
 CTONG3000084, CTONG3000657, CTONG3002127, D3OST3000169,
 35 DFNES2001108, DFNES2011499, FCBBF3007540, HCASM2001301,
 HCHON2000028, HCHON2006250, HHDPC1000118, HLUNG2001996,

HLUNG2002465, KIDNE2001847, MESAN2006563, NHNPC2001816,
 NT2NE2003252, NT2RI2005166, NT2RI3000622, NT2RI3006673,
 NT2RP7005118, NT2RP7005529, NT2RP7009147, NT2RP7013795,
 NT2RP8000483, NTONG2003852, OCBBF2004826, OCBBF2004883,
 5 OCBBF2007028, OCBBF2008770, OCBBF2022351, OCBBF2037340,
 OCBBF2037547, PEBLM2004666, PLACE7008431, PROST2016462,
 PROST2018511, PUAEN2002616, PUAEN2005930, PUAEN2006328,
 PUAEN2009852, SYNOV2021320, TESOP2000801, TESOP2001166,
 TESTI2006648, TESTI2026505, TESTI2050137, TESTI2052693,
 10 TESTI4000079, TESTI4010713, TESTI4010831, TESTI4011956,
 TESTI4016882, TESTI4019843, TESTI4028059, THYMU2032014,
 THYMU2037226, THYMU2038615, THYMU3001234, THYMU3006172,
 THYMU3008436, TLIVE2009541, TRACH2009310, TRACH2021398,
 TRACH2023299, TRACH2025535, TRACH3009455, TRACH3034731,
 15 TSTOM2000553, UTERU1000337, UTERU2005621, UTERU2025025,
 UTERU2036089, UTERU2038251, UTERU3003523, UTERU3007419

The following 38 clones are also predicted to belong to the category of signal transduction-related protein.

BLADE2000579, BRACE3001058, BRACE3003053, BRACE3009127,
 20 BRAMY2040159, BRAMY3004800, BRAWH3009017, BRCAN2014229,
 BRHIP2026877, BRTHA2013610, CTONG3004550, FEBRA2001990,
 FEBRA2008692, HCHON2000508, MESAN2001770, NT2RI2005772,
 NT2RI3007443, NTONG2008093, OCBBF2005433, OCBBF2024284,
 OCBBF2034637, OCBBF3002654, TESOP2000390, TESTI2025924,
 25 TESTI2049956, TESTI4000319, TESTI4005317, TESTI4021482,
 TESTI4025268, TESTI4031745, THYMU2004139, THYMU2031249,
 TRACH2024408, UTERU2008040, UTERU2028734, UTERU3000402,
 UTERU3000738, UTERU3015412

The clones predicted to belong to the category of transcription-related protein are the following 27 clones.

BRACE2006319, BRACE3013576, BRAMY2030109, BRAWH3005912,
 BRHIP3025161, CORDB1000140, CTONG1000467, HEART2001756,
 IMR322000127, IMR322000917, KIDNE1000064, NOVAR2000136,
 NT2NE2006531, NT2RI3007158, NT2RP7000466, OCBBF2036743,
 35 OCBBF3009279, PLACE6019385, TESTI2026505, TESTI2044796,

TESTI2050987, TESTI4017001, TESTI4019140, TESTI4034912,
THYMU2035735, TRACH2025749, TRACH3004840

The following 88 clones are also predicted to belong to the category of transcription-related protein.

5. BRACE2003609, BRACE3001058, BRACE3001113, BRACE3003026,
BRAMY2035070, BRAMY2035449, BRAMY2035718, BRAMY2039341,
BRAMY2045471, BRAWH3007441, BRHIP2017553, BRSTN2013354,
CERVX2002013, CTONG1000113, CTONG2003348, CTONG2020374,
CTONG2020378, CTONG2020411, CTONG2024031, CTONG2028758,
10 CTONG3001501, CTONG3004726, DFNES2011192, FCBBF3027854,
FEBRA2014122, FEBRA2027609, HCASM2003018, HCASM2003099,
HCHON2000508, HCHON2000743, HCHON2004858, HSYRA2005628,
MESAN2014412, MESAN2015501, NT2RI2008952, NT2RI2018448,
NT2RI3000174, NT2RI3001132, NT2RI3002557, NT2RI3007167,
15 NT2RI3007443, OCBBF2008144, OCBBF2009583, OCBBF2011669,
OCBBF2019684, OCBBF2020048, OCBBF2024284, OCBBF2032274,
OCBBF3000167, OCBBF3003761, SPLEN2016135, SPLEN2016781,
SPLEN2036702, SYNOV2021953, SYNOV4002744, TESOP2001796,
TESOP2005199, TESOP2006398, TESTI2008901, TESTI2034251,
20 TESTI2037830, TESTI4000183, TESTI4000214, TESTI4006473,
TESTI4008058, TESTI4008302, TESTI4013365, TESTI4014801,
TESTI4015442, TESTI4017714, TESTI4025494, TESTI4025547,
TESTI4028938, TESTI4029348, TESTI4031745, TESTI4032090,
THYMU2006001, THYMU2028739, THYMU2031139, THYMU3001428,
25 TRACH2007483, TRACH3000134, TRACH3003832, TRACH3007866,
UTERU3001053, UTERU3014791, UTERU3017176, TESTI4038779

The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following 176 clones.

3NB692002806, ASTRO1000009, BLADE2005036, BLADE2008539,
30 BRACE2005457, BRACE2008594, BRACE2014475, BRACE2018762,
BRACE2035381, BRACE2043142, BRACE2047011, BRACE3004058,
BRACE3007625, BRACE3009708, BRACE3011421, BRACE3015262,
BRACE3024073, BRACE3025630, BRACE3027478, BRAMY2047746,
BRAMY2047751, BRAMY3002803, BRAMY3004919, BRAMY3005091,
35 BRAMY4000095, BRAWH2010000, BRAWH2014414, BRAWH2014662,
BRAWH2016702, BRAWH3002821, BRAWH3003727, BRCAN2021028,

BRCAN2024451, BRCAN2028355, BRCOC2003213, BRHIP2004359,
 BRHIP2026288, BRHIP3008183, BRHIP3025161, BRHIP3027137,
 BRSSN2000684, BRSTN2000872, BRSTN2004863, BRSTN2004987,
 BRTHA2012980, BRTHA3002401, BRTHA3008778, BRTHA3009037,
 5 BRTHA3009090, BRTHA3015815, BRTHA3016917, BRTHA3017848,
 BRTHA3018656, COLON2001721, CTONG2004062, CTONG2006798,
 CTONG2013178, CTONG2028124, CTONG3002127, CTONG3005325,
 CTONG3005648, D3OST2002182, FCBBF3004502, FCBBF3013307,
 FEBRA2007708, FEBRA2008468, FEBRA2026984, HCASM2001301,
 10 HCASM2002918, HCHON2002676, HCHON2004007, HCHON2004531,
 HEART2006131, HHDPC1000118, HLUNG1000017, KIDNE2000832,
 KIDNE2006580, MESAN2012054, NOVAR2000136, NT2NE2003252,
 NT2NE2006909, NT2RI2004618, NT2RI3004510, NT2RI3006673,
 NT2RI3007978, NT2RI3008652, NT2RP7010599, NT2RP7014005,
 15 NT2RP7017474, NTONG2000413, OCBBF2004826, OCBBF2006058,
 OCBBF2019823, OCBBF2025527, OCBBF2031167, OCBBF2037340,
 OCBBF2037547, OCBBF2037638, PERIC2009086, PLACE7002641,
 PLACE7008431, PROST2017367, PUAEN2007044, PUAEN2009795,
 PUAEN2009852, SPLEN2010912, SPLEN2015679, SPLEN2030335,
 20 SYNOV4002392, SYNOV4002883, TBAES2003550, TESOP2000801,
 TESOP2004114, TESOP2009121, TESTI1000257, TESTI1000545,
 TESTI2002618, TESTI2006648, TESTI2040018, TESTI2049469,
 TESTI2053621, TESTI4000288, TESTI4000349, TESTI4001148,
 TESTI4001527, TESTI4001561, TESTI4002552, TESTI4006819,
 25 TESTI4007382, TESTI4007810, TESTI4008429, TESTI4010713,
 TESTI4010851, TESTI4012448, TESTI4012679, TESTI4013369,
 TESTI4016925, TESTI4018835, TESTI4020920, TESTI4021478,
 TESTI4022716, TESTI4026510, TESTI4028059, TESTI4029836,
 TESTI4032895, TESTI4034432, TESTI4036909, THYMU2006420,
 30 THYMU3000133, THYMU3001379, THYMU3004835, THYMU3006172,
 THYMU3008436, TLIVE2002336, TRACH2006387, TRACH2009310,
 TRACH2019473, TRACH2022425, TRACH2023299, TRACH3005479,
 TRACH3006470, TRACH3007479, TRACH3008093, TRACH3008629,
 TRACH3036193, TSTOM2000553, UTERU2005621, UTERU2017762,
 35 UTERU2025025, UTERU2033375, UTERU3000828, UTERU3001240,
 UTERU3001585, UTERU3003116, UTERU3005460, UTERU3005907

The following 89 clones are also predicted to belong to the category of enzyme and/or metabolism-related protein.

BLADE2000579, BRACE2039823, BRACE3003053, BRAMY2038516,
 BRAMY2040159, BRAWH1000369, BRCAN2003070, BRCAN2014229,
 5 BRROC2019841, BRHIP2005724, BRHIP2008389, BRHIP2026877,
 BRHIP3000240, BRHIP3026052, BRTHA2002133, BRTHA2002702,
 BRTHA2007060, BRTHA2010033, BRTHA2013426, BRTHA2013610,
 BRTHA2017364, BRTHA2018011, BRTHA3000296, CTONG2004000,
 CTONG2016942, CTONG2020374, CTONG2024031, CTONG3002552,
 10 CTONG3003598, CTONG3004550, FCBBF1000509, FEBRA2008692,
 HCASM2002754, HCASM2003099, HCASM2003357, HLUNG2015418,
 HLUNG2015548, IMR322013731, MESAN2005303, NT2RI2005772,
 NT2RI2008952, NT2RI3000174, NT2RI3007443, NT2RP7008435,
 NTONG2008093, OCBBF2006987, OCBBF2034637, OCBBF3002654,
 15 PLACE7000333, PLACE7000502, PROST2000452, SPLEN2039311,
 STOMA2003158, SYNOV2013637, TESOP2000390, TESTI2015626,
 TESTI2025924, TESTI2026647, TESTI2035981, TESTI2036288,
 TESTI2039060, TESTI2049956, TESTI4000155, TESTI4001984,
 TESTI4006473, TESTI4010382, TESTI4011072, TESTI4014801,
 20 TESTI4017714, TESTI4021482, TESTI4025547, TESTI4025865,
 TESTI4026207, TESTI4028958, TESTI4029690, TESTI4031745,
 TESTI4032090, THYMU2004139, THYMU2031139, THYMU2031249,
 THYMU2040925, TKIDN2012771, TLIVE2002046, TLIVE2007607,
 TRACH3000420, TRACH3007866, UTERU2019534, UTERU2028734,
 25 UTERU3000738

The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following ten clones.

BRAWH2001940, CTONG3001123, HCHON2001217, PROST2008993,
 30 TBAES2001171, TESTI4021294, TESTI4035498, UTERU1000024,
 UTERU3002993, UTERU3003523

The following three clones are also predicted to belong to the category of cell division and/or cell proliferation-related protein.

35 BRACE2029396, BRAWH2010552, TESTI4013365

The clones predicted to belong to the category of cytoskeleton-related protein are the following 36 clones.

BRACE2026836, BRACE2045300, BRAWH3000314, BRSTN2004863,
 BRTHA2004978, BRTHA3003449, BRTHA3005046, COLON2002520,
 5 CORDB2000541, CTONG3002674, FCBBF3012288, HCHON2001577,
 HLUNG2017350, HSYRA2005456, HSYRA2009075, NT2RI3006340,
 NT2RI3006673, NT2RI3007291, OCBBF2037598, PLACE5000282,
 TESTI2003347, TESTI2034767, TESTI4000288, TESTI4007778,
 TESTI4009160, TESTI4018886, TESTI4030603, TESTI4034632,
 10 TESTI4035063, THYMU1000496, THYMU2008725, TRACH2005811,
 TRACH2007059, UTERU2007724, UTERU2035745, UTERU3004616

The following four clones are also predicted to belong to the category of cytoskeleton-related protein.

NT2RI2005772, OCBBF2006987, SPLEN2030847, TESTI4026207

15 The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 20 clones.

BRACE3024073, BRAWH2001940, BRCOC2003213, BRSTN2004987,
 BRTHA3016917, CTONG3009028, FCBBF3013307, FEBRA2026984,
 20 SPLEN2010912, TBAES2001171, TESTI2040018, TESTI4019566,
 TESTI4022716, TESTI4026510, TESTI4036909, THYMU3000133,
 TRACH2023299, TRACH3036193, UTERU1000024, UTERU3002993

The following eleven clones are also predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein.

BRACE3003053, BRCAN2002473, BRTHA2017364, NT2RI2008952,
 NT2RI3000174, TESTI2026647, TESTI2035981, TESTI4000155,
 TESTI4006473, TESTI4010382, TESTI4025547

25 The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 29 clones.

BRACE2014306, BRACE3008720, BRAWH3000491, BRCAN2009432,
 BRHIP2000920, BRTHA3013884, CTONG2013178, HCHON2004531,
 HLUNG1000017, HLUNG2013851, HSYRA2005496, NT2NE2006909,
 35 NT2RI3006340, OCBBF2007068, OCBBF2031167, PUAEN2009795,
 TBAES2001229, TBAES2004055, TESTI2051867, TESTI4000014,

TESTI4000349, TESTI4009608, TESTI4010851, TESTI4034632,
TRACH3007479, TRACH3036193, UTERU2017762, UTERU2019940,
UTERU2033375

The following 17 clones are also predicted to belong to the
category of protein synthesis and/or transport-related protein.

BLADE2000579, BRACE3003053, BRCAN2003070, BRTHA2018011,
BRTHA3000296, CTONG2016942, MESAN2005303, NT2RI3002557,
NT2RP7008435, PERIC2007068, PLACE7000502, PROST2000452,
TESTI4001984, TESTI4017714, THYMU2004284, TRACH3000420,

TRACH3007866

The clones predicted to belong to the category of cellular
defense-related protein are the following four clones.

BRTHA2015878, CTONG3000084, NT2RI3002842, PEBLM2004666

The following three clones are also predicted to belong to
the category of cellular defense-related protein.

BRCAN2002473, NT2RI3007167, TRACH3002561

The clones predicted to belong to the category of
development and/or differentiation-related protein are the
following one clone.

TESTI4014924

The clones predicted to belong to the category of DNA-
binding and/or RNA-binding protein are the following 67 clones.

BRACE2006319, BRACE2047011, BRACE3004150, BRACE3013576,
BRACE3024073, BRAMY2030109, BRAWH3005912, BRCAN2002562,

BRCOC2003213, BRHIP2021615, BRHIP3008183, BRHIP3025161,

BRSTN2004987, BRTHA2018707, BRTHA3016917, CORDB1000140,

CTONG1000467, CTONG3000084, CTONG3003972, CTONG3008831,

CTONG3009028, FCBBF3013307, FEBRA2026984, HEART2001756,

HLUNG2013851, IMR322000127, IMR322000917, KIDNE1000064,

NT2NE2006531, NT2RI3003382, NT2RI3007158, NT2RP7000466,

NT2RP7004123, OCBBF2036743, OCBBF3009279, PLACE6019385,

SPLEN2006122, SPLEN2010912, TESOP2009121, TESTI1000390,

TESTI2014716, TESTI2026505, TESTI2040018, TESTI2044796,

TESTI2050987, TESTI4007810, TESTI4009374, TESTI4011745,

TESTI4012679, TESTI4017001, TESTI4019140, TESTI4019566,

TESTI4022716, TESTI4026510, TESTI4034432, TESTI4034912,

TESTI4036909, THYMU2035319, THYMU2035735, THYMU3000133,
 TLIVE2002336, TRACH2023299, TRACH2025749, TRACH3004840,
 TRACH3036193, UTERU2026025, UTERU3009490

The following 112 clones are also predicted to belong to
 5 the category of DNA-binding and/or RNA-binding protein.
 BLADE2006830, BRACE2003609, BRACE3001058, BRACE3001113,
 BRACE3003026, BRACE3003053, BRACE3010076, BRAMY2035070,
 BRAMY2035449, BRAMY2039341, BRAMY2045471, BRAWH1000369,
 BRAWH3007441, BRHIP2017553, BRSTN2013354, BRTHA2002133,
 10 BRTHA2002702, BRTHA2017364, BRTHA2017972, CERVX2002013,
 CTONG1000113, CTONG2003348, CTONG2015596, CTONG2020374,
 CTONG2020378, CTONG2020411, CTONG2024031, CTONG2028758,
 CTONG3001501, CTONG3004726, DFNES2011192, FCBBF1000509,
 FCBBF3027854, FEBRA2014122, FEBRA2027609, HCASM2003018,
 15 HCASM2003099, HCASM2009424, HCHON2000508, HCHON2000743,
 HCHON2004858, HSYRA2005628, IMR322013731, MESAN2014412,
 MESAN2015501, NT2RI2008952, NT2RI2018448, NT2RI2027157,
 NT2RI3000174, NT2RI3001132, NT2RI3002557, NT2RI3007167,
 NT2RI3007443, OCBBF2006987, OCBBF2008144, OCBBF2009583,
 20 OCBBF2011669, OCBBF2019684, OCBBF2020048, OCBBF2024284,
 OCBBF2032274, OCBBF2034637, OCBBF3000167, OCBBF3003761,
 PERIC2007068, SPLEN2016135, SPLEN2016781, SPLEN2036702,
 STOMA2003158, SYNOV2021953, SYNOV4002744, TESOP2001796,
 TESOP2005199, TESOP2006398, TESTI2008901, TESTI2026647,
 25 TESTI2034251, TESTI2035981, TESTI2037830, TESTI4000155,
 TESTI4000183, TESTI4000214, TESTI4006473, TESTI4008058,
 TESTI4008302, TESTI4010382, TESTI4013365, TESTI4014801,
 TESTI4015442, TESTI4017714, TESTI4025494, TESTI4025547,
 TESTI4026207, TESTI4028938, TESTI4028958, TESTI4029348,
 30 TESTI4031745, TESTI4032090, THYMU2006001, THYMU2028739,
 THYMU2031139, THYMU3001428, TKIDN2012771, TLIVE2007607,
 TRACH2007483, TRACH3000134, TRACH3003832, TRACH3007866,
 UTERU3001053, UTERU3014791, UTERU3017176, TESTI4038779

The clones predicted to belong to the category of ATP
 35 binding and/or GTP-binding protein are the following 28 clones.

BRACE3008720, BRACE3009708, BRAMY2047746, BRAMY3004919,
 BRAWH2014662, BRAWH2016702, BRCAN2009432, BRCAN2024451,
 BRSTN2013741, BRTHA3008778, BRTHA3009090, CTONG2004062,
 CTONG2028124, HCHON2004007, OCBBF2037340, SPLEN2030335,
 5 TESTI4000288, TESTI4001148, TESTI4002552, TESTI4008429,
 TESTI4018835, TESTI4021478, TESTI4029836, THYMU2036459,
 THYMU3001379, TRACH2001549, UTERU3000828, UTERU3001240

The following eight clones are also predicted to belong to the category of ATP binding and/or GTP-binding protein.

10 BRCAN2014229, BRHIP2008389, CTONG3004550, FEBRA2001990,
 IMR322013396, IMR322013731, MESAN2001770, TESTI4000319

The following 208 clones have hit data in Pfam (see Example 5), and each has a functional domain or motif. It is currently unclear as to which of the above-described categories each of
 15 these clones belong. However, if data on polypeptides with a similar domain or motif can be accumulated, and their functions clarified in more detail, they may be classified into any of the above-described categories.

3NB692002685, 3NB692008729, ASTRO2003960, BNGH42003570,
 20 BRACE2010489, BRACE2015314, BRACE2016981, BRACE2027258,
 BRACE2030341, BRACE2035441, BRACE2038329, BRACE2042550,
 BRACE2044286, BRACE3000071, BRACE3000973, BRACE3001002,
 BRACE3003192, BRACE3004772, BRACE3004880, BRACE3008137,
 BRACE3008384, BRACE3009090, BRACE3010397, BRACE3015521,
 25 BRACE3016884, BRACE3019084, BRAMY2004771, BRAMY2019300,
 BRAMY2021498, BRAMY2031317, BRAMY2039872, BRAMY2046989,
 BRAMY3004224, BRAMY3005932, BRAWH1000127, BRAWH2001395,
 BRAWH2014954, BRAWH3000078, BRAWH3001891, BRAWH3002574,
 BRAWH3002600, BRAWH3008341, BRCAN2002948, BRCAN2009203,
 30 BRCAN2015464, BRCAN2017717, BRCOC2001505, BRCOC2016525,
 BRHIP2003786, BRHIP2005236, BRHIP2007616, BRHIP2009414,
 BRHIP3000339, BRHIP3008313, BRSTN2001067, BRTHA2000855,
 BRTHA2005579, BRTHA2007122, BRTHA2008527, BRTHA2009311,
 BRTHA2010884, BRTHA2013262, BRTHA2014792, BRTHA2015406,
 35 BRTHA2016496, BRTHA2018591, BRTHA2018624, BRTHA2019048,
 BRTHA3003074, BRTHA3008310, CTONG1000341, CTONG2001877,

CTONG2008233, CTONG2017500, CTONG2020026, CTONG2028687,
 CTONG3000686, CTONG3004072, CTONG3006067, CTONG3006186,
 CTONG3009385, DFNES2000146, DFNES2005266, FCBBF3009888,
 FCBBF3012170, FEBRA2000253, FEBRA2007801, FEBRA2021571,
 5 FEBRA2024150, HCHON2004776, HEART1000139, HEART2006909,
 HEART2010495, HLUNG2000014, HLUNG2002958, HLUNG2011298,
 IMR322006495, KIDNE2000846, KIDNE2001361, KIDNE2011635,
 KIDNE2012945, NESOP2001656, NT2RI2008724, NT2RI2025909,
 NT2RI2025957, NT2RI3007543, NT2RP7000359, NT2RP7004027,
 10 NT2RP7011570, NT2RP8000296, NTONG2005277, NTONG2006354,
 NTONG2007517, OCBBF2006764, OCBBF2010416, OCBBF2020838,
 OCBBF2021323, OCBBF2033869, PERIC2001228, PERIC2003720,
 PLACE6020031, PLACE7000514, PROST2018090, RECTM2000433,
 SKMUS2006394, SMINT1000192, SPLEN2002147, SPLEN2002467,
 15 SPLEN2031780, SPLEN2034081, SPLEN2036821, SYNOV2005448,
 SYNOV2005817, SYNOV2006430, SYNOV2014400, SYNOV4007553,
 SYNOV4008440, TESOP2001953, TESTI2000443, TESTI2004700,
 TESTI2027019, TESTI4000462, TESTI4000970, TESTI4002491,
 TESTI4006546, TESTI4007064, TESTI4011484, TESTI4012406,
 20 TESTI4015471, TESTI4016110, TESTI4017137, TESTI4017575,
 TESTI4018152, TESTI4018555, TESTI4020092, TESTI4023555,
 TESTI4025920, TESTI4026192, TESTI4027557, TESTI4028429,
 TESTI4028612, TESTI4028983, TESTI4030505, TESTI4038492,
 TESTI4039659, TESTI4041053, TESTI4044084, TESTI4046487,
 25 TESTI4046819, THYMU2004693, THYMU2011736, THYMU2016204,
 THYMU2027734, THYMU2038369, THYMU2038797, THYMU3000028,
 THYMU3003212, THYMU3003763, THYMU3007137, THYMU3008171,
 TLIVE2002338, TLIVE2002690, TLIVE2003225, TLIVE2008229,
 TRACH2001443, TRACH3001427, TRACH3003379, TRACH3008713,
 30 TRACH3035235, TUTER2000425, UTERU1000031, UTERU2006115,
 UTERU2006568, UTERU2019706, UTERU2035328, UTERU2035331,
 UTERU2035452, UTERU3001652, UTERU3001766, UTERU3001988,
 UTERU3002667, UTERU3003178, UTERU3005585, UTERU3007640,
 UTERU3008660, UTERU3009871, UTERU3009979, UTERU3015500

35 Likewise, the following 45 clones also had hit data in Pfam
 (see Example 5), although it remains unclear as to which of the

above-described categories each clone belongs. When data on polypeptides with a similar domain or motif are accumulated, and their functions are clarified in more detail, these clones may also be classified into any of the above-described categories.

- 5 3NB692004724// KRAB box// Integrase core domain
ADRGL2000042// Nucleosome assembly protein (NAP)
BRACE2037299// Integrase core domain
BRALZ2017844// Homeobox domain
BRAWH2006207// KRAB box
- 10 BRCAN2002854// SAP domain
BRHIP2006617// TPR Domain// TPR Domain
BRHIP2012360// XPG N-terminal domain// XPG I-region
BRHIP3008314// Sir2 family
BRTHA2016318// KE2 family protein
- 15 CTONG2019822// Hepatitis C virus core protein
FCBBF3010361// Fork head domain
FEBRA2006519// Thrombospondin type 1 domain// Thrombospondin type 1 domain
FEBRA2028256// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// TB domain// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// EB module// Squash family of serine protease inhibitors// EGF-like domain// EGF-like domain
FEBRA2028516// GRIP domain
- 25 HCASM2008536// XRCC1 N terminal domain
IMR322007078// UBA domain
IMR322008651// Helix-hairpin-helix motif.
LIVER2000247// Sodium
OCBBF2003327// Thrombospondin type 1 domain// Thrombospondin type 1 domain// Thrombospondin type 1 domain
- 30 PROST2009320// LIM domain containing proteins// LIM domain containing proteins
PUAEN2006335// Formin Homology 2 Domain
SKMUS2003194// SAP domain
- 35 SPLEN2039379// Transthyretin precursor (formerly prealbumin)
SYNOV1000256// Leucine Rich Repeat// BAH domain// Leucine Rich

Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 SYNOV2006620// Nuclear transition protein 2
 SYNOV4003981// Somatomedin B domain// WAP-type (Whey Acidic Protein) 'four-disulfide core'// Hemopexin// Hemopexin
 5 SYNOV4005889// Apolipoprotein A1/A4/E family
 TESOP2006865// KRAB box
 TESTI1000266// Integrase core domain
 TESTI2050780// Kazal-type serine protease inhibitor domain
 TESTI4000137// Domain of unknown function
 10 TESTI4024387// GDP dissociation inhibitor
 TESTI4029528// RanBP1 domain.
 TESTI4038721// Squash family of serine protease inhibitors
 TESTI4046240// Sir2 family
 THYMU2035078// Domain of unknown function DUF27
 15 THYMU3000269// FAD binding domain
 THYMU3000360// Integrase core domain
 TRACH1000212// TSC-22/dip/bun family
 TRACH2000862// Guanylate-binding protein
 TRACH2019672// CRAL/TRIO domain.
 20 TRACH2024559// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 UTERU2032279// Serpins (serine protease inhibitors)
 UTERU2033577// KRAB box

The function of a motif or domain may sometimes belong to
 25 more than one of the above-described functional categories, and
 there is also the possibility that such a motif or domain may be
 predicted to belong to every functional category. As new
 polypeptide data are accumulated and novel domains and motifs
 are found, a new functional domain or motif may be identified by
 30 re-analyzing deduced amino acid sequences in homology searches
 using updated databases. Thus in the future, the remaining
 clones, for which there are currently no hit data, may be
 classified into any of the above-described categories.

Since the polypeptides encoded by clones of the present
 35 invention contain full-length amino acid sequences, it is
 possible to analyze their biological activity and effect on

cellular conditions such as cell proliferation and differentiation, by expressing the polypeptides as recombinant polypeptides using an appropriate expression system, injecting the recombinant into a cell, or raising a specific antibody
5 against that polypeptide.

The biological activities of respective polypeptides can be analyzed by the methods as shown below.

Secretory protein, transmembrane protein:

"Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical
10 Approach Series" (IRL PRESS),
"Growth Factors" (Eds., I. McKay, I. Leigh, 1993),
"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The
15 Practical Approach Series" (IRL PRESS),
"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F. Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

20 Signal transduction-related protein:

"Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),
"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or
"Signal Transduction Protocols" (Eds., David A. Kendall,
25 Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

Transcription-related protein:

"Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),
30 "Transcription Factors" (Ed., D. S. Latchman, 1993);

Enzyme and/or metabolism-related protein:

"Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS);

Cell division and/or cell proliferation-related protein:

"Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

- 5 "Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),

"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana Press) series;

- 10 Nuclear protein and/or RNA synthesis-related protein:

"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),

"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

- 15 Protein synthesis and/or transport-related protein:

"Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS),

- 20 "Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

Cellular defense-related protein:

"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,

"Chaperonin Protocols" (Eds., Schneider, Christine, 2000);

- 25 Development and/or differentiation-related protein:

"Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

- 30 "DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,

"RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

- 35 ATP- and/or GTP-binding protein:

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

5 When other techniques are used, the activity of a polypeptide can be analyzed according to the description in Methods in Enzymology (Academic Press).

10 In the above-described categorization, a clone predicted to belong to the secretory and/or membrane protein category refers to a clone having hit data in a homology search with some annotation to suggest that the clone encodes a secretory and/or membrane protein, such as a growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, and connective tissue
15 protein; or a clone in which the results of PSORT and SOSUI analyses for deduced ORF suggest the presence of a nucleotide sequence encoding a signal sequence or transmembrane region; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains/motifs that suggest receptors,
20 ion channels, hormones, or growth factors, for example, seven-transmembrane receptors, pancreatic hormone peptides, ion transport proteins, or fibroblast growth factors.

A clone predicted to belong to the glycoprotein-related protein category means a clone having hit data in a homology
25 search with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein; or a clone in which the results of a domain/motif search with Pfam indicate the presence of domains and motifs such as a glycoprotein or glycosyltransferase that suggest the involvement
30 of glycobiology, for example, immunoglobulin domain or glycosyl transferases group 1.

A clone predicted to belong to the signal transduction-related protein category means a clone having hit data in a homology search with some annotation, such as serine/threonine-
35 protein kinase, tyrosine-protein kinase, SH3 domain, and SH2 domain, suggesting that the clone encodes a signal transduction-

related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest a protein kinase, dephosphoenzyme, SH2 domain, or small G protein, for example, eukaryotic protein kinase domain, protein phosphatase 2C, or Ras family.

A clone predicted to belong to the transcription-related protein category means a clone having hit data in a homology search with some annotation, such as transcription regulation, zinc finger, and homeobox, suggesting that the clone encodes a transcription-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest a transcription factor or transcription-controlling protein, for example, bZIP transcription factor, Zinc finger, or C2H2 type.

A clone predicted to belong to the category of disease-related protein means a clone having hit data in a homology search with some annotation, such as disease mutation and syndrome, suggesting that the clone encodes a disease-related protein; or a clone whose full-length nucleotide sequence has hit data in Swiss-Prot, GenBank, UniGene, nr or RefSeq, where that hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), the human gene and disease database described later; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs, that suggest proteins with disease-specific expression or proteins involved in increasing or decreasing expression (depending on the disease), for example, Wilm's tumor protein or von Hippel-Lindau disease tumor suppressor protein.

A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data in a homology search with some annotation, such as metabolism, oxidoreductase, and E. C. No. (Enzyme commission number), suggesting that the clone encodes an enzyme and/or metabolism-related protein; or a clone in which the results of a domain/motif search with Pfam suggests the presence of domains

and motifs that suggest transferase, synthase, or hydrolase, for example, aldehyde dehydrogenase family, chitin synthase, or glucose-6-phosphate dehydrogenase.

5 A clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data in a homology search with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, and apoptosis, suggesting that the clone encodes a cell division and/or cell proliferation-related protein; or a clone
10 in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest cyclin or cell proliferation-controlling protein, for example, cyclin or cell division protein.

A clone predicted to belong to the category of
15 cytoskeleton-related protein means a clone having hit data in a homology search with some annotation, such as structural protein, cytoskeleton, actin-binding, and microtubules, suggesting that the clone encodes a cytoskeleton-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the
20 presence of domains and motifs that suggest actin, kinesin, or fibronectin, for example, actin, fibronectin type I domain, or kinesin motor domain.

A clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone
25 having hit data in a homology search with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, and polyadenylation, suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the
30 presence of domains and motifs that suggest splicing factor, RNA synthase, or helicase, for example, hepatitis C virus RNA dependent RNA polymerase or DEAD/DEAH box helicase.

A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having
35 hit data in a homology search with some annotation, such as translation regulation, protein biosynthesis, amino-acid

biosynthesis, ribosomal protein, protein transport, and signal recognition particle, suggesting that the clone encodes a protein synthesis and/or transport-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest translation-relating protein, ubiquitin-relating protein, or ribosomal protein, for example, translation initiation factor SUI1, ubiquitin family, or ribosomal protein L16.

A clone predicted to belong to the category of cellular defense-related protein means a clone having hit data in a homology search with some annotation, such as heat shock, DNA repair, and DNA damage, suggesting that the clone encodes a cellular defense-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest chaperonin or DNA repair protein, for example, HSP90 protein or DNA mismatch repair protein.

A clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data in a homology search with some annotation, such as developmental protein, suggesting that the clone encodes a development and/or differentiation-related protein; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest organogenesis-relating protein, for example, floricaula/leafy protein.

A clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having hit data in a homology search with some annotation, such as DNA-binding, RNA-binding, and such; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest DNA/RNA-relating enzyme group including transcription factor and DNA ligase or Zinc-finger relating protein, for example, transcription factor WhiB, B-box zinc finger, or tRNA synthetases class I (C).

A clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having hit data in a homology

search with some annotation, such as ATP-binding, GTP-binding, and such; or a clone in which the results of a domain/motif search with Pfam suggest the presence of domains and motifs that suggest ATP/GTP-relating enzyme group including ATPase or G protein, for example, E1-E2 ATPase or Ras family.

It is possible to perform functional analysis of a protein involved in a disease as described above. It is also possible to analyze correlation between a protein's expression or activity and a certain disease by using a specific antibody obtained by using the expressed protein. Alternatively, it is possible to utilize the OMIM database, which is a database of human genes and diseases, to analyze the protein. New information is constantly being deposited into this database. Therefore, it is possible that one skilled in the art will find a new relationship between a particular disease and a gene of the present invention by using the most up-to-date database. Proteins involved in diseases are useful for developing diagnostic markers or medicines for regulation of their expression and activity, or as gene therapy targets.

The proteins may have a variety of functions, including but not limited to the above 14 categories, such as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, or transcription-related proteins. When searching OMIM using these keywords, the proteins are revealed to be involved in a great number of diseases (the results of the OMIM search for secretory and membrane proteins are shown below as an Example). Associations between proteins related to signal transduction or transcription and diseases are reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). As another example and as described in "Biology of Cancer", many proteins are involved in cancers, including enzymes and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins,

membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, (S. Matsubara, 1992) of Life Science series (Shokabo). As the above example clearly demonstrates, not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, and transcription-related proteins are often involved in diseases, and thus such proteins can be useful targets in the field of medical industry.

The results of the OMIM search for secretory and membrane proteins are shown below. The keywords used were:

- (1) secretion protein,
- (2) membrane protein,
- (3) channel, and
- (4) extracellular matrix.

Only the OMIM accession numbers are shown in the search results. The first 50 accession numbers displayed in the search results are provided. Using this number, data showing the relationship between a disease and a gene or protein can be seen. OMIM data is renewed daily.

1) Secretion protein

When searching under these keywords, 436 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

*604667, *104760, *176860, *139320, *118910, *151675, *107400,
 *604029, #200100, *177061, *600946, *601693, *139250, *176880,
 *600998, *603850, *605083, *147572, *179513, *606055, *604028,
 *125950, *157147, *246700, *602926, *600560, *602421, *603215,
 185860, *600174, *179512, *109270, *179511, *179510, *179509,
 *601146, *604710, *177020, *138120, *170280, *600626, *164160,
 *168470, *154545, *603831, *601652, *104311, *601489, *603062,
 *102720

2) Membrane protein

When searching under these keywords, 1873 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

5 *130500, *605704, *305360, *153330, *109270, *173610, *170995,
 *120920, *170993, *309060, *104776, *602333, *605703, *602690,
 *605943, *159430, *600897, *606867, *133090, *601178, *602413,
 *602003, *604405, *605940, *603237, *109280, *606958, *600378,
 *606959, *602173, *107776, *602334, *125305, *602335, *309845,
 *601134, *605731, *606795, *185881, *607178, *603177, *154045,
 10 *603214, *603718, *606909, *600594, *603241, *606629, *603657,
 *600182

3) Channel (member of membrane proteins)

15 When searching under these keywords, 449 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

*176266, *600724, *605427, *182390, *123825, *114208, *114206,
 *114205, *176267, *600053, *601784, *603749, *182392, *600937,
 *603415, *114204, *114209, *114207, *607370, *604528, *604527,
 20 *601011, *600760, *192500, *118425, *600228, *600359, *176261,
 *602235, *600761, *182389, *300008, *600877, *605692, *300338,
 *602232, *603537, *182391, *176263, *602343, *601328, *605874,
 *604385, *603939, *602208, *601534, *601958, *603220, *600504,
 *607368

25

4) Extracellular matrix

When searching under these keywords, 267 genes were registered as being associated with disease. The OMIM numbers for 50 of these genes are as follows.

30 *605912, *602201, *603479, *604633, *601418, *601548, *115437,
 *154870, *120361, *602285, *600754, *602262, *134797, *602261,
 *603320, *603321, *604871, *604629, *601807, #154700, *128239,
 *600310, *605470, *185250, *178990, *603767, *120360, *185261,
 *116935, *607056, *253700, *190180, *600985, *188826, *193300,
 35 *276901, *308700, *120150, *602109, *120324, *600514, #177170,

#247100, #116920, #200610, *605127, *601313, *601652, *120180, *154790

In addition to these, various keywords shown in the above-mentioned categorizations or others can be used in an OMIM search to reveal involvement in disease.

Further, the use of nucleotide sequences of cDNAs of the present invention enables the expression frequency of genes corresponding to those cDNAs to be analyzed. Gene function can be predicted based on information obtained by expression frequency analysis.

There are several methods for analyzing the expression level of genes involved in disease. Differences in gene expression levels between diseased and normal tissues can be studied by analytical methods using, for example, Northern blotting, RT-PCR, DNA microarrays, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujunsha (2000)). In addition to these analysis methods, computer analysis can be used to compare the nucleotide sequences of expressed genes, and hence to analyze expression frequency. For example, in the "BODYMAP" database, gene clones are randomly extracted from cDNA libraries of various tissues and/or cells, clones homologous to each other are assigned to a single cluster based on 3'-end nucleotide sequence homology information, genes are then classified into clusters, and the number of clones in each cluster is compared to gain information on expression frequency (<http://bodymap.ims.u-tokyo.ac.jp/>).

When these analytical methods result in observation of an explicit difference between gene expression levels in diseased tissues and normal tissues, it can be concluded that the gene is closely involved in the disease or disorder. When gene expression is explicitly different between normal cells and cells reproducing specific disease-associated features, even if they are not diseased tissues, it can be concluded that the gene is closely involved in a disease or disorder.

Of the 2,495 clones whose full-length nucleotide sequences were revealed, genes involved in a particular pathology or function were selected using the database shown below (see Example 7; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains the nucleotide sequences of 1,402,069 clones, a sufficiently large population for analysis. Sequence information in the database was obtained by randomly selecting cDNA clones from cDNA libraries derived from the various tissues and cells shown in Example 1, and determining the 5'-end sequences thereof.

The nucleotide sequence of each clone in this database was then categorized (clustered) based on nucleotide sequence homology determined with a search program. The number of clones belonging to each cluster of each library was determined and normalized; and the ratio of a certain gene in a cDNA library was determined. This analysis provided information on the expression frequency of a gene in the tissue or cell that was the source of the cDNA library.

In order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells, which had been used in large-scale cDNA analyses, were taken as subjects for comparison of expression levels between different tissues or cells. Namely, expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which were derived the 600 or more cDNA clones whose nucleotide sequences had been analyzed. This analysis showed that the cDNA clones corresponded to the genes involved in the pathologies and functions indicated below. Each value in Tables 2 to 24 indicated below represents a relative expression frequency; a higher value indicates a higher expression level. Genes included in these Tables do not indicate such a big difference between compared libraries, but when compared with other tissue- or gene-derived libraries based on Example 9, they indicate a significant difference. Thus, these genes are specific to a tissue or cell, and can be considered useful

diagnostic markers for disease, as well as useful for analyzing molecular mechanisms.

Osteoporosis-related genes

5 Osteoporosis is a pathology in which bones are easily broken owing to an overall decrease in bone components. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Genes involved in the increase of osteoclasts
10 differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are thus genes involved in osteoporosis relevant to bone metabolism.

Nucleotide sequence-based analysis was carried out to identify genes whose expression frequencies were higher or lower
15 in CD34+ cells (cells expressing glycoprotein CD34) treated with osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)), compared to untreated CD34+ cells, which are precursor cells in monocyte/macrophage lines. The result of comparative analysis of frequency between the cDNA libraries
20 prepared from the RNA of CD34+ cells (CD34C), and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) (Table 2), showed that the genes whose expression levels differed between the two were 15 and two clones indicated below.

25 BRACE3013780, BRAMY2047420, BRSTN2016470, CTONG3008894, D3OST2002182, D3OST2002648, D3OST3000169, PEBLM2005183, PUAEN2009655, TESTI4000014, TESTI4010851, TRACH2023299, TRACH2025535, TRACH3001427, UTERU2006137
HCHON2000508, TESTI2015626

30 These clones are involved in osteoporosis.

Genes involved in neural cell differentiation

Genes involved in neural cell differentiation are useful for treating neurological disease. Genes with varying
35 expression levels in response to induction of cellular

differentiation in neural cells are thought to be involved in neurological disease.

A survey was performed for genes whose expression levels varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and cells subjected to differentiation treatment (NT2RP, NT2RI or NT2NE) (Table 3) showed that the genes whose expression levels differed between the two were 174 and 30 clones indicated below.

BNGH42007788, BRACE1000186, BRACE2006319, BRACE2014306,
BRACE2015058, BRACE2044286, BRACE3010428, BRAMY2044078,
BRAWH2014645, BRAWH2014662, BRAWH3002574, BRAWH3003992,
BRAWH3005981, BRAWH3007592, BRCAN2009432, BRCAN2016619,
BRCAN2028355, BRHIP2001074, BRHIP2007741, BRHIP2014228,
BRHIP2024146, BRHIP3007586, BRHIP3018797, BRTHA2003461,
BRTHA3000633, BRTHA3003490, COLON2001721, CTONG1000087,
CTONG2008233, CTONG2020638, CTONG2028124, CTONG3003905,
CTONG3008894, CTONG3009028, CTONG3009239, DFNES2011499,
FCBBF3001977, FEBRA1000030, FEBRA2006396, FEBRA2007801,
HCHON2000028, HCHON2000244, HCHON2001084, HCHON2001217,
HCHON2001548, HCHON2006250, HEART1000074, HHDPC1000118,
HSYRA2009075, IMR322000127, IMR322001380, KIDNE2000665,
KIDNE2002252, MESAN2006563, MESAN2012054, MESAN2015515,
NT2NE2003252, NT2NE2005890, NT2NE2006531, NT2NE2006909,
NT2NE2008060, NT2RI2003993, NT2RI2004618, NT2RI2005166,
NT2RI2006686, NT2RI2008724, NT2RI2009855, NT2RI2011422,
NT2RI2011683, NT2RI2012659, NT2RI2012990, NT2RI2013357,
NT2RI2014247, NT2RI2014551, NT2RI2014733, NT2RI2016128,
NT2RI2018311, NT2RI2018883, NT2RI2019751, NT2RI2023303,
NT2RI2025909, NT2RI2025957, NT2RI2027081, NT2RI2027396,
NT2RI3000622, NT2RI3001263, NT2RI3001515, NT2RI3002303,
NT2RI3002842, NT2RI3002892, NT2RI3003031, NT2RI3003095,
NT2RI3003162, NT2RI3003382, NT2RI3003409, NT2RI3004381,
NT2RI3004510, NT2RI3005202, NT2RI3005403, NT2RI3005724,

NT2RI3006132, NT2RI3006171, NT2RI3006284, NT2RI3006340,
 NT2RI3006376, NT2RI3006673, NT2RI3006796, NT2RI3007065,
 NT2RI3007158, NT2RI3007291, NT2RI3007543, NT2RI3007757,
 NT2RI3007978, NT2RI3008055, NT2RI3008162, NT2RI3008652,
 5 NT2RI3008697, NT2RI3008974, NT2RI3009158, NT2RP7000359,
 NT2RP7000466, NT2RP7004027, NT2RP7004123, NT2RP7005118,
 NT2RP7005529, NT2RP7005846, NT2RP7009030, NT2RP7009147,
 NT2RP7009867, NT2RP7010128, NT2RP7010599, NT2RP7011570,
 NT2RP7013795, NT2RP7014005, NT2RP7015512, NT2RP7017365,
 10 NT2RP7017474, NT2RP7017546, NT2RP8000137, NT2RP8000296,
 NT2RP8000483, NTONG2005969, OCBBF2007028, OCBBF2037068,
 PLACE7000514, PUAEN2007044, SPLEN2002467, SPLEN2006122,
 SPLEN2028914, SPLEN2031547, SYNOV4002346, SYNOV4007671,
 SYNOV4008440, TESOP2002273, TESTI2003573, TESTI4000014,
 15 TESTI4009286, TESTI4010851, TESTI4012702, TESTI4029671,
 TESTI4037156, THYMU3000133, TRACH1000205, TRACH2005811,
 TRACH2007834, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004721, TRACH3008093, TRACH3008535, TRACH3008713,
 UTERU2002410, UTERU2023175
 20 ADRGL2000042, BRACE2003609, BRACE3003026, BRHIP3000017,
 CTONG2020411, FCBBF1000509, FCBBF3027854, FEBRA2028516,
 HCHON2000508, IMR322001879, NT2RI2005772, NT2RI2008952,
 NT2RI2009583, NT2RI2018448, NT2RI2027157, NT2RI3000174,
 NT2RI3001132, NT2RI3002557, NT2RI3005928, NT2RI3007167,
 25 NT2RI3007443, NT2RP7008435, NT2RP8000521, OCBBF2006987,
 PERIC2007068, TESTI2015626, TESTI4015442, TLIVE2002046,
 TRACH3000134, TUTER2000057

These genes are neurological disease-related genes.

30 Genes involved in Alzheimer's disease

Alzheimer's disease is a cranial neurological disease
 characterized by memory loss. As the disease advances, patients
 can no longer support themselves and require nursing.
 Alzheimer's disease eventually leads to brain atrophication.

35 Environmental factors such as stress, and vascular factors such
 as hypertension and cholesterolemia, are assumed but not

confirmed to contribute to the onset of Alzheimer's disease. Genes whose expression levels differ between normal brain tissues and tissues affected with Alzheimer's disease are expected to be involved in Alzheimer's disease. Such genes can
 5 be used to elucidate the disease's onset mechanism and in genetic diagnosis. cDNA libraries derived from the cerebral cortex of Alzheimer patients (BRALZ and BRASW) and a library derived from the whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 4). Genes whose expression levels
 10 differed between the two were the 250 clones and 41 clones listed below.

ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 BRACE1000533, BRACE2005457, BRACE2010489, BRACE2014657,
 BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,
 15 BRACE3003192, BRACE3005499, BRACE3007480, BRACE3009237,
 BRACE3009724, BRACE3009747, BRACE3010428, BRACE3011271,
 BRACE3011421, BRACE3012364, BRACE3022769, BRACE3026735,
 BRACE3031838, BRALZ2011796, BRALZ2012183, BRALZ2012848,
 BRALZ2014484, BRALZ2016085, BRALZ2016498, BRALZ2017359,
 20 BRAMY2003008, BRAMY2005052, BRAMY2019300, BRAMY2019963,
 BRAMY2036567, BRAMY2037823, BRAMY2040592, BRAMY3002803,
 BRAMY3004224, BRAMY3005091, BRASW1000053, BRASW1000125,
 BRAWH1000127, BRAWH2001395, BRAWH2001671, BRAWH2001940,
 BRAWH2001973, BRAWH2002560, BRAWH2002761, BRAWH2005315,
 25 BRAWH2007658, BRAWH2010000, BRAWH2010084, BRAWH2010536,
 BRAWH2012162, BRAWH2012326, BRAWH2013294, BRAWH2013871,
 BRAWH2014414, BRAWH2014645, BRAWH2014662, BRAWH2014876,
 BRAWH2014954, BRAWH2016221, BRAWH2016439, BRAWH2016702,
 BRAWH2016724, BRAWH3000078, BRAWH3000100, BRAWH3000314,
 30 BRAWH3000491, BRAWH3001326, BRAWH3001475, BRAWH3001891,
 BRAWH3002574, BRAWH3002600, BRAWH3002819, BRAWH3002821,
 BRAWH3003522, BRAWH3003555, BRAWH3003727, BRAWH3003801,
 BRAWH3003992, BRAWH3004453, BRAWH3004666, BRAWH3005132,
 BRAWH3005422, BRAWH3005912, BRAWH3005981, BRAWH3006548,
 35 BRAWH3006792, BRAWH3007221, BRAWH3007506, BRAWH3007592,
 BRAWH3007726, BRAWH3007783, BRAWH3008341, BRAWH3008697,

BRAWH3008931, BRAWH3009297, BRCOC2003213, BRCOC2014033,
BRCOC2020142, BRHIP2000920, BRHIP2005719, BRHIP2007741,
BRHIP2014228, BRHIP2024146, BRHIP2026288, BRHIP3000339,
BRHIP3006683, BRHIP3007586, BRHIP3008405, BRHIP3018797,
5 BRSSN2000684, BRSSN2011738, BRSSN2014299, BRSTN2008052,
BRSTN2015015, BRSTN2016470, BRTHA1000311, BRTHA2008335,
BRTHA3002427, BRTHA3003490, BRTHA3008520, BRTHA3017848,
COLON2001721, CTONG2017500, CTONG2028124, CTONG3000657,
CTONG3001123, CTONG3009328, FCBBF2001183, FCBBF3001977,
10 FEBRA2007544, FEBRA2007801, FEBRA2020886, FEBRA2028618,
HCASM2007047, HCHON2000244, HCHON2000626, HCHON2001217,
HCHON2002676, HCHON2006250, HEART1000074, HHDP1000118,
HLUNG2002465, IMR322000127, IMR322001380, IMR322002035,
KIDNE2006580, MESAN2006563, MESAN2012054, MESTC1000042,
15 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
NT2RI2014733, NT2RI3002892, NT2RI3006284, NT2RI3006673,
NT2RI3007543, NT2RI3008055, NT2RP7005529, NT2RP7009147,
NT2RP7014005, NT2RP7017474, NTONG2005969, OCBBF2001794,
OCBBF2006005, OCBBF2006764, OCBBF2007028, OCBBF2007114,
20 OCBBF2010140, OCBBF2021286, OCBBF2023162, OCBBF2024850,
OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,
PUAEN2006701, PUAEN2007044, PUAEN2009655, SMINT2001818,
SPLEN2028914, SPLEN2031424, SPLEN2031547, SPLEN2034781,
25 SPLEN2036932, SYNOV2014400, SYNOV4002346, SYNOV4002883,
SYNOV4007430, SYNOV4007671, SYNOV4008440, TESOP2002273,
TESOP2002451, TESTI4000014, TESTI4000209, TESTI4001100,
TESTI4006137, TESTI4008797, TESTI4009286, TESTI4010851,
TESTI4013817, TESTI4014694, TESTI4021478, TESTI4022936,
30 TESTI4024420, TESTI4027821, THYMU2001090, THYMU2033308,
THYMU2035735, THYMU2039315, THYMU3001234, THYMU3008171,
TKIDN2009641, TKIDN2009889, TKIDN2015788, TRACH1000205,
TRACH2001549, TRACH2005811, TRACH2006049, TRACH2007834,
TRACH2008300, TRACH2025535, TRACH3001427, TRACH3002192,
35 TRACH3004068, TRACH3004721, TRACH3005294, TRACH3007479,
TRACH3008093, TRACH3009455, UTERU2005621, UTERU2006115,

UTERU2019706, UTERU2023039, UTERU2026203, UTERU3005230,
 UTERU3007640, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRALZ2017844,
 BRAMY3004800, BRAWH1000369, BRAWH2006207, BRAWH2006395,
 5 BRAWH2008993, BRAWH2009393, BRAWH2010552, BRAWH3007441,
 BRAWH3009017, BRHIP2005271, BRHIP3000017, BRHIP3026052,
 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000743, IMR322001879, NT2RI2009583,
 10 OCBBF2008144, PERIC2007068, PUAEN2006335, SPLEN2039379,
 TESTI4001984, TESTI4008058, TESTI4025268, TESTI4032090,
 THYMU3000360, TLIVE2002046, TRACH3000134, UTERU2021820,
 UTERU2028734

These genes are involved in Alzheimer's disease.

15

Genes involved in Parkinson's disease

Parkinson's disease is a cranial neurological disease
 characterized by impaired production of the neurotransmitter
 dopamine in the substantia nigra in the brain. This results in
 20 dyskinesia, such as hand tremors, and impaired body movement due
 to muscular rigidity. Normally, the number of brain neurons
 gradually decreases with age. However, compared to healthy
 people, patients with Parkinson's disease experience a rapid and
 marked decrease in the number of neurons in their substantia
 25 nigra. Genes whose expression levels differ between tissues of
 the whole brain and the nigra are expected to be involved in
 Parkinson's disease. These genes exhibit nigra-specific
 alterations in their expression levels, and can be used to
 elucidate the disease onset mechanism and in gene diagnosis.
 30 cDNA libraries derived from the substantia nigra (BRSSN) and a
 library derived from whole tissues of a normal brain (BRAWH)
 were analyzed and compared (Table 5). Genes whose expression
 levels differed between the two were the 250 clones and 40
 clones listed below.
 35 ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 BRACE1000533, BRACE2005457, BRACE2010489, BRACE2014657,

BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,
 BRACE3003192, BRACE3005499, BRACE3007480, BRACE3009237,
 BRACE3009724, BRACE3009747, BRACE3010428, BRACE3011271,
 BRACE3011421, BRACE3012364, BRACE3013780, BRACE3022769,
 5 BRACE3026735, BRACE3031838, BRALZ2011796, BRAMY2003008,
 BRAMY2005052, BRAMY2019300, BRAMY2019963, BRAMY2036567,
 BRAMY2037823, BRAMY2040592, BRAMY2047420, BRAMY3002803,
 BRAMY3004224, BRAMY3005091, BRAWH1000127, BRAWH2001395,
 BRAWH2001671, BRAWH2001940, BRAWH2001973, BRAWH2002560,
 10 BRAWH2002761, BRAWH2005315, BRAWH2007658, BRAWH2010000,
 BRAWH2010084, BRAWH2010536, BRAWH2012162, BRAWH2012326,
 BRAWH2013294, BRAWH2013871, BRAWH2014414, BRAWH2014645,
 BRAWH2014662, BRAWH2014876, BRAWH2014954, BRAWH2016221,
 BRAWH2016439, BRAWH2016702, BRAWH2016724, BRAWH3000078,
 15 BRAWH3000100, BRAWH3000314, BRAWH3000491, BRAWH3001326,
 BRAWH3001475, BRAWH3001891, BRAWH3002574, BRAWH3002600,
 BRAWH3002819, BRAWH3002821, BRAWH3003522, BRAWH3003555,
 BRAWH3003727, BRAWH3003801, BRAWH3003992, BRAWH3004453,
 BRAWH3004666, BRAWH3005132, BRAWH3005422, BRAWH3005912,
 20 BRAWH3005981, BRAWH3006548, BRAWH3006792, BRAWH3007221,
 BRAWH3007506, BRAWH3007592, BRAWH3007726, BRAWH3007783,
 BRAWH3008341, BRAWH3008697, BRAWH3008931, BRAWH3009297,
 BRCOC2003213, BRCOC2014033, BRCOC2020142, BRHIP2000920,
 BRHIP2005719, BRHIP2007741, BRHIP2014228, BRHIP2024146,
 25 BRHIP3000339, BRHIP3006683, BRHIP3007586, BRHIP3008405,
 BRHIP3018797, BRSSN2000684, BRSSN2003086, BRSSN2004496,
 BRSSN2004719, BRSSN2006892, BRSSN2008549, BRSSN2008797,
 BRSSN2011262, BRSSN2011738, BRSSN2013874, BRSSN2014299,
 BRSSN2014424, BRSSN2014556, BRSSN2018581, BRSSN2018925,
 30 BRSTN2008052, BRSTN2015015, BRSTN2016470, BRTHA1000311,
 BRTHA2003461, BRTHA2008335, BRTHA3002427, BRTHA3003490,
 BRTHA3008520, BRTHA3017848, COLON2001721, CTONG2017500,
 CTONG2028124, CTONG3000657, CTONG3001123, CTONG3009328,
 FCBBF2001183, FCBBF3001977, FEBRA2007544, FEBRA2007801,
 35 FEBRA2020886, FEBRA2024136, FEBRA2025427, FEBRA2028618,
 HCASM2007047, HCHON2000244, HCHON2000626, HCHON2001217,

HCHON2002676, HCHON2006250, HEART1000074, HHDPCL000118,
 HLUNG2002465, IMR322000127, IMR322002035, KIDNE2006580,
 MESAN2006563, MESAN2012054, MESTC1000042, NOVAR2001783,
 NT2NE2006909, NT2RI2008724, NT2RI2012659, NT2RI2014733,
 5 NT2RI3002892, NT2RI3006284, NT2RI3006673, NT2RI3007543,
 NT2RI3008055, NT2RP7005529, NT2RP7009147, NT2RP7014005,
 NT2RP7017474, OCBBF2001794, OCBBF2006005, OCBBF2006764,
 OCBBF2007028, OCBBF2010140, OCBBF2021286, OCBBF2024850,
 OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
 10 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,
 PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2028914,
 SPLEN2031424, SPLEN2031547, SPLEN2034781, SPLEN2036932,
 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4008440, TESOP2002451, TESTI4000014, TESTI4000209,
 15 TESTI4001100, TESTI4006137, TESTI4008797, TESTI4009286,
 TESTI4010851, TESTI4013817, TESTI4014694, TESTI4021478,
 TESTI4022936, TESTI4024420, TESTI4027821, TESTI4037156,
 THYMU2001090, THYMU2033308, THYMU2035735, THYMU2039315,
 THYMU3001234, THYMU3008171, TKIDN2009641, TKIDN2009889,
 20 TKIDN2015788, TRACH1000205, TRACH2001549, TRACH2005811,
 TRACH2006049, TRACH2007834, TRACH2008300, TRACH2025535,
 TRACH3001427, TRACH3002192, TRACH3004721, TRACH3005294,
 TRACH3007479, TRACH3008093, TRACH3009455, UTERU2006115,
 UTERU2019706, UTERU2023039, UTERU2026203, UTERU3005230,
 25 UTERU3007640, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRHIP2005271, BRHIP3000017, BRTHA2018443, BRTHA3003000,
 30 CTONG2020374, CTONG2020378, CTONG2024031, FCBBF1000509,
 FEBRA2001990, FEBRA2006519, FEBRA2028516, HCHON2000743,
 IMR322001879, NT2RI2009583, OCBBF2008144, PERIC2007068,
 PUAEN2006335, SPLEN2039379, TESTI2015626, TESTI4001984,
 TESTI4008058, TESTI4025268, TESTI4032090, THYMU3000360,
 35 TLIVE2002046, TRACH3000134, UTERU2021820, UTERU2028734

These genes are involved in Parkinson's disease.

Genes involved in short-term memory and dementia

In the brain, the hippocampus is a highly important memory-related area. The hippocampus functions to establish a memory by judging whether acquired information is necessary, and then accumulating the memory in another area of the brain. According to clinical findings, patients can retain a new memory for only about five minutes with an abnormal, or at worst without a hippocampus. Some dementia patients are presumed to have hippocampus abnormalities. Thus, genes whose expression levels differ between tissues of the whole brain and the hippocampus are expected to be involved in memory or dementia. Such genes can be used to elucidate the mechanism underlying memory, and in gene diagnosis. cDNA libraries derived from the hippocampus (BRHIP) and from the whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 6). Genes whose expression levels differed between the two were the 370 clones and 59 clones listed below.

ASTRO1000009, BLADE2001371, BLADE2008398, BNGH42007788,
 BRACE1000186, BRACE1000258, BRACE1000533, BRACE2005457,
 BRACE2010489, BRACE2014657, BRACE2015058, BRACE2018762,
 BRACE2030341, BRACE2035381, BRACE2044286, BRACE2045954,
 BRACE3000787, BRACE3003192, BRACE3005499, BRACE3007480,
 BRACE3009237, BRACE3009724, BRACE3009747, BRACE3010428,
 BRACE3011271, BRACE3011421, BRACE3012364, BRACE3018963,
 BRACE3022769, BRACE3026735, BRACE3031838, BRALZ2011796,
 BRAMY2003008, BRAMY2005052, BRAMY2019300, BRAMY2019963,
 BRAMY2031317, BRAMY2036567, BRAMY2037823, BRAMY2040592,
 BRAMY2044078, BRAMY3002803, BRAMY3004224, BRAMY3005091,
 BRAWH1000127, BRAWH2001395, BRAWH2001671,
 BRAWH2001940, BRAWH2001973, BRAWH2002560, BRAWH2002761,
 BRAWH2005315, BRAWH2007658, BRAWH2010000, BRAWH2010084,
 BRAWH2010536, BRAWH2012162, BRAWH2012326, BRAWH2013294,
 BRAWH2013871, BRAWH2014414, BRAWH2014645, BRAWH2014662,
 BRAWH2014876, BRAWH2014954, BRAWH2016221, BRAWH2016439,
 BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,

BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
BRAWH3003801, BRAWH3003992, BRAWH3004453, BRAWH3004666,
5 BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
BRAWH3006548, BRAWH3006792, BRAWH3007221, BRAWH3007506,
BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2020710,
BRCAN2028355, BRCOC2003213, BRCOC2014033, BRCOC2020142,
10 BRHIP2000691, BRHIP2000819, BRHIP2000826, BRHIP2000920,
BRHIP2001074, BRHIP2001805, BRHIP2001927, BRHIP2002122,
BRHIP2002172, BRHIP2002346, BRHIP2003242, BRHIP2003786,
BRHIP2003917, BRHIP2004312, BRHIP2004359, BRHIP2004814,
BRHIP2004883, BRHIP2005236, BRHIP2005354, BRHIP2005600,
15 BRHIP2005719, BRHIP2005752, BRHIP2005932, BRHIP2006800,
BRHIP2007616, BRHIP2007741, BRHIP2009340, BRHIP2009414,
BRHIP2009474, BRHIP2013699, BRHIP2014228, BRHIP2021615,
BRHIP2022221, BRHIP2024146, BRHIP2024165, BRHIP2026061,
BRHIP2026288, BRHIP2029176, BRHIP2029393, BRHIP3000339,
20 BRHIP3000526, BRHIP3001283, BRHIP3006683, BRHIP3007483,
BRHIP3007586, BRHIP3008183, BRHIP3008313, BRHIP3008344,
BRHIP3008405, BRHIP3008565, BRHIP3008598, BRHIP3008997,
BRHIP3009099, BRHIP3009448, BRHIP3011241, BRHIP3013765,
BRHIP3013897, BRHIP3015751, BRHIP3016213, BRHIP3018797,
25 BRHIP3020182, BRHIP3024118, BRHIP3024533, BRHIP3024725,
BRHIP3025161, BRHIP3025702, BRHIP3026097, BRHIP3027137,
BRHIP3027854, BRSSN2000684, BRSSN2004719, BRSSN2008549,
BRSSN2011738, BRSSN2014299, BRSTN2008052, BRSTN2015015,
BRSTN2016470, BRSTN2018083, BRTHA1000311, BRTHA2002442,
30 BRTHA2008335, BRTHA3000297, BRTHA3001721, BRTHA3002427,
BRTHA3003490, BRTHA3005046, BRTHA3008520, BRTHA3008778,
BRTHA3009090, BRTHA3015910, BRTHA3017848, COLON2001721,
CTONG1000087, CTONG1000088, CTONG1000467, CTONG2000042,
CTONG2008233, CTONG2009423, CTONG2017500, CTONG2019788,
35 CTONG2028124, CTONG3000657, CTONG3001123, CTONG3001370,
CTONG3002412, CTONG3004072, CTONG3008894, CTONG3009239,

CTONG3009328, DFNES2011499, FCBBF2001183, FCBBF3001977,
 FEBRA2000253, FEBRA2007544, FEBRA2007801, FEBRA2008287,
 FEBRA2010719, FEBRA2020886, FEBRA2028618, HCASM2007047,
 HCHON2000028, HCHON2000244, HCHON2000626, HCHON2001217,
 5 HCHON2002676, HCHON2005921, HCHON2006250, HEART1000074,
 HEART2007031, HHDPC1000118, HLUNG2002465, HLUNG2003003,
 IMR322000127, IMR322001380, IMR322002035, KIDNE2005543,
 KIDNE2006580, MESAN2006563, MESAN2012054, MESTC1000042,
 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
 10 NT2RI2014733, NT2RI2018311, NT2RI3001515, NT2RI3002892,
 NT2RI3004510, NT2RI3005724, NT2RI3006284, NT2RI3006673,
 NT2RI3007291, NT2RI3007543, NT2RI3008055, NT2RP7005529,
 NT2RP7009147, NT2RP7014005, NT2RP7017474, OCBBF2001794,
 OCBBF2003819, OCBBF2006005, OCBBF2006151, OCBBF2006764,
 15 OCBBF2007028, OCBBF2007068, OCBBF2010140, OCBBF2020741,
 OCBBF2021286, OCBBF2024719, OCBBF2024850, OCBBF2028935,
 OCBBF2036743, OCBBF2038317, OCBBF3000296, OCBBF3000483,
 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,
 PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2010912,
 20 SPLEN2012624, SPLEN2028914, SPLEN2031424, SPLEN2031547,
 SPLEN2034781, SPLEN2036932, SYNOV2014400, SYNOV4002346,
 SYNOV4002883, SYNOV4007430, SYNOV4008440, TESOP2002451,
 TESTI2049246, TESTI4000014, TESTI4000209, TESTI4001100,
 TESTI4006137, TESTI4008797, TESTI4009286, TESTI4010377,
 25 TESTI4010851, TESTI4010928, TESTI4011161, TESTI4013817,
 TESTI4014159, TESTI4014694, TESTI4014818, TESTI4021478,
 TESTI4022936, TESTI4024420, TESTI4027821, TESTI4037156,
 THYMU2001090, THYMU2023967, THYMU2025707, THYMU2031341,
 THYMU2033308, THYMU2035735, THYMU2037226, THYMU2039315,
 30 THYMU3001234, THYMU3001379, THYMU3004835, THYMU3007137,
 THYMU3008171, TKIDN2009641, TKIDN2009889, TKIDN2015788,
 TRACH1000205, TRACH2001549, TRACH2005811, TRACH2006049,
 TRACH2007834, TRACH2008300, TRACH2025535, TRACH3000014,
 TRACH3001427, TRACH3002192, TRACH3004721, TRACH3005294,
 35 TRACH3007479, TRACH3008093, TRACH3009455, TUTER1000122,
 TUTER2000904, UTERU2004929, UTERU2006115, UTERU2019706,

UTERU2021163, UTERU2023039, UTERU2026203, UTERU2030213,
 UTERU3001572, UTERU3003135, UTERU3005230, UTERU3007640,
 UTERU3009259, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 5 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRHIP2002722, BRHIP2003272, BRHIP2005271, BRHIP2005724,
 BRHIP2006617, BRHIP2008389, BRHIP2012360, BRHIP2017553,
 BRHIP2026877, BRHIP3000017, BRHIP3000240, BRHIP3008314,
 10 BRHIP3026052, BRTHA2018443, BRTHA3003000, CTONG2020374,
 CTONG2020378, CTONG2024031, CTONG3004726, FCBBF1000509,
 FEBRA2001990, FEBRA2006519, FEBRA2028516, HCHON2000743,
 IMR322001879, NT2RI2009583, OCBBF2006987, OCBBF2008144,
 OCBBF2030116, PERIC2007068, PUAEN2006335, SPLEN2039379,
 15 TESTI2015626, TESTI4000214, TESTI4001984, TESTI4008058,
 TESTI4013894, TESTI4025268, TESTI4025547, TESTI4026207,
 TESTI4032090, THYMU3000360, TLIVE2002046, TRACH3000134,
 UTERU2008040, UTERU2021820, UTERU2028734

These genes are involved in memory and dementia.

20

Genes involved in equilibrium sense and movement function

The cerebellum is the center of equilibrium sense, muscular
 movement, and motor learning. This area is thought to be
 involved in motor control, and smooth movements are achieved
 25 unconsciously due to cerebellum action. Recent studies have
 elucidated that the cerebellum participates in not only simple
 movements but also in establishing higher-order movements such
 as reading and writing. Thus, genes whose expression levels
 differ between tissues of the whole brain and the cerebellum are
 30 expected to be involved in equilibrium sense or motor function,
 which can be useful for elucidating the molecular mechanism
 controlled by the brain. cDNA libraries derived from the
 cerebellum (BRACE) and from the whole tissues of a normal brain
 (BRAWH) were analyzed and compared (Table 7). Genes whose
 35 expression levels differed between the two were the 488 clones
 and 66 clones listed below.

ADRGL2009146, ADRGL2012038, ASTRO1000009, ASTRO2003960,
BLADE1000176, BLADE2004089, BLADE2008398, BRACE1000186,
BRACE1000258, BRACE1000533, BRACE1000572, BRACE2003639,
BRACE2005457, BRACE2006319, BRACE2008594, BRACE2010489,
5 BRACE2011747, BRACE2014306, BRACE2014475, BRACE2014657,
BRACE2015058, BRACE2015314, BRACE2016981, BRACE2018762,
BRACE2024627, BRACE2026836, BRACE2027258, BRACE2027970,
BRACE2028970, BRACE2029112, BRACE2029849, BRACE2030326,
BRACE2030341, BRACE2030884, BRACE2031154, BRACE2031389,
10 BRACE2031527, BRACE2031531, BRACE2031899, BRACE2032044,
BRACE2032329, BRACE2032385, BRACE2032538, BRACE2032823,
BRACE2033720, BRACE2035381, BRACE2035441, BRACE2036005,
BRACE2036096, BRACE2036830, BRACE2036834, BRACE2037847,
BRACE2038114, BRACE2038329, BRACE2038551, BRACE2039249,
15 BRACE2039327, BRACE2039475, BRACE2039734, BRACE2040138,
BRACE2040325, BRACE2041009, BRACE2041200, BRACE2041264,
BRACE2042550, BRACE2043142, BRACE2043248, BRACE2043349,
BRACE2043665, BRACE2044286, BRACE2044816, BRACE2044949,
BRACE2045300, BRACE2045428, BRACE2045596, BRACE2045772,
20 BRACE2045947, BRACE2045954, BRACE2046251, BRACE2046295,
BRACE2047011, BRACE2047350, BRACE2047377, BRACE2047385,
BRACE3000071, BRACE3000697, BRACE3000787, BRACE3000840,
BRACE3000973, BRACE3001002, BRACE3001217, BRACE3001391,
BRACE3001595, BRACE3001754, BRACE3002298, BRACE3002390,
25 BRACE3002508, BRACE3003004, BRACE3003192, BRACE3003595,
BRACE3003698, BRACE3004058, BRACE3004113, BRACE3004150,
BRACE3004358, BRACE3004435, BRACE3004772, BRACE3004783,
BRACE3004843, BRACE3004880, BRACE3005145, BRACE3005225,
BRACE3005430, BRACE3005499, BRACE3006185, BRACE3006226,
30 BRACE3006462, BRACE3006872, BRACE3007322, BRACE3007472,
BRACE3007480, BRACE3007559, BRACE3007625, BRACE3007642,
BRACE3007767, BRACE3008036, BRACE3008092, BRACE3008137,
BRACE3008384, BRACE3008720, BRACE3008772, BRACE3009090,
BRACE3009237, BRACE3009297, BRACE3009377, BRACE3009574,
35 BRACE3009701, BRACE3009708, BRACE3009724, BRACE3009747,
BRACE3010397, BRACE3010428, BRACE3011271, BRACE3011421,

BRACE3011505, BRACE3012364, BRACE3012930, BRACE3013119,
BRACE3013576, BRACE3013740, BRACE3013780, BRACE3014005,
BRACE3014068, BRACE3014231, BRACE3014317, BRACE3014807,
BRACE3015027, BRACE3015121, BRACE3015262, BRACE3015521,
5 BRACE3015894, BRACE3016884, BRACE3018308, BRACE3018963,
BRACE3019055, BRACE3019084, BRACE3020194, BRACE3020286,
BRACE3020594, BRACE3022769, BRACE3023912, BRACE3024073,
BRACE3024659, BRACE3024662, BRACE3025153, BRACE3025457,
BRACE3025531, BRACE3025630, BRACE3026008, BRACE3026075,
10 BRACE3026735, BRACE3027242, BRACE3027326, BRACE3027478,
BRACE3030103, BRACE3031838, BRACE3032983, BRACE3040856,
BRACE3045033, BRALZ2011796, BRAMY2003008, BRAMY2005052,
BRAMY2019300, BRAMY2019963, BRAMY2020058, BRAMY2030098,
BRAMY2031317, BRAMY2036567, BRAMY2037823, BRAMY2039872,
15 BRAMY2040592, BRAMY2044078, BRAMY2047420, BRAMY3002620,
BRAMY3002803, BRAMY3004224, BRAMY3005091, BRAMY3005932,
BRAMY4000229, BRAWH1000127, BRAWH2001395, BRAWH2001671,
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20 BRAWH2010536, BRAWH2012162, BRAWH2012326, BRAWH2013294,
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BRAWH2014876, BRAWH2014954, BRAWH2016221, BRAWH2016439,
BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,
BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
25 BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
BRAWH3003801, BRAWH3003992, BRAWH3004453, BRAWH3004666,
BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
BRAWH3006548, BRAWH3006792, BRAWH3007221, BRAWH3007506,
30 BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2009432,
BRCAN2010376, BRCAN2015371, BRCAN2020710, BRCOC2003213,
BRCOC2007034, BRCOC2014033, BRCOC2020142, BRHIP2000920,
BRHIP2004359, BRHIP2005719, BRHIP2005752, BRHIP2007741,
35 BRHIP2013699, BRHIP2014228, BRHIP2024146, BRHIP3000339,
BRHIP3006683, BRHIP3007586, BRHIP3008313, BRHIP3008405,

BRHIP3018797, BRSSN2000684, BRSSN2006892, BRSSN2011262,
 BRSSN2011738, BRSSN2014299, BRSTN2008052, BRSTN2010750,
 BRSTN2015015, BRSTN2016470, BRTHA1000311, BRTHA2008335,
 BRTHA2008955, BRTHA2011194, BRTHA3001721, BRTHA3002427,
 5 BRTHA3003490, BRTHA3008520, BRTHA3009090, BRTHA3017848,
 COLON2001721, CTONG2008233, CTONG2017500, CTONG2028124,
 CTONG3000657, CTONG3001123, CTONG3005813, CTONG3008894,
 CTONG3009328, DFNES2011499, FCBBF2001183, FCBBF3001977,
 FEBRA2006396, FEBRA2007544, FEBRA2007708, FEBRA2007801,
 10 FEBRA2008287, FEBRA2020886, FEBRA2021966, FEBRA2026984,
 FEBRA2028618, HCASM2007047, HCHON2000244, HCHON2000626,
 HCHON2001217, HCHON2002676, HCHON2005921, HCHON2006250,
 HEART1000074, HHDPC1000118, HLUNG2002465, IMR322000127,
 IMR322001380, IMR322002035, KIDNE2000665, KIDNE2006580,
 15 MESAN2006563, MESAN2012054, MESTC1000042, NB9N41000340,
 NESOP2001752, NOVAR2001783, NT2NE2006909, NT2RI2005166,
 NT2RI2008724, NT2RI2012659, NT2RI2014733, NT2RI2019751,
 NT2RI3002892, NT2RI3003382, NT2RI3004510, NT2RI3005724,
 NT2RI3006284, NT2RI3006673, NT2RI3007291, NT2RI3007543,
 20 NT2RI3008055, NT2RP7004123, NT2RP7005529, NT2RP7009147,
 NT2RP7010599, NT2RP7014005, NT2RP7017474, NTONG2005969,
 OCBBF2001794, OCBBF2003819, OCBBF2006005, OCBBF2006151,
 OCBBF2006764, OCBBF2007028, OCBBF2010140, OCBBF2020343,
 OCBBF2020741, OCBBF2021286, OCBBF2022351, OCBBF2024850,
 25 OCBBF2025527, OCBBF2028935, OCBBF2036743, OCBBF2038317,
 OCBBF3000483, OCBBF3007516, OCBBF3008230, PEBLM2004666,
 PERIC2000889, PLACE6001185, PUAEN2002489, PUAEN2005930,
 PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2010912,
 SPLEN2012624, SPLEN2027268, SPLEN2028914, SPLEN2031424,
 30 SPLEN2031547, SPLEN2034781, SPLEN2036932, SPLEN2037194,
 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4007671, SYNOV4008440, TESOP2002273, TESOP2002451,
 TESOP2002950, TESTI1000330, TESTI4000014, TESTI4000209,
 TESTI4000349, TESTI4001100, TESTI4001561, TESTI4006137,
 35 TESTI4008797, TESTI4009286, TESTI4010851, TESTI4011161,
 TESTI4013675, TESTI4013817, TESTI4014159, TESTI4014306,

TESTI4014694, TESTI4021478, TESTI4022936, TESTI4024420,
 TESTI4027821, TESTI4037156, TESTI4046819, THYMU2001090,
 THYMU2016523, THYMU2023967, THYMU2030264, THYMU2033308,
 THYMU2035735, THYMU2039315, THYMU2039780, THYMU3001083,
 5 THYMU3001234, THYMU3003309, THYMU3006485, THYMU3008171,
 TKIDN2009641, TKIDN2009889, TKIDN2015788, TRACH1000205,
 TRACH2001549, TRACH2005811, TRACH2006049, TRACH2007834,
 TRACH2008300, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004721, TRACH3005294, TRACH3006038, TRACH3006412,
 10 TRACH3007479, TRACH3008093, TRACH3009455, TUTER2000904,
 UTERU2002410, UTERU2006115, UTERU2007520, UTERU2019706,
 UTERU2023039, UTERU2026203, UTERU3000226, UTERU3001572,
 UTERU3005230, UTERU3005460, UTERU3005970, UTERU3006308,
 UTERU3007419, UTERU3007640, UTERU3007913, UTERU3009871
 15 ADRGL2000042, BLADE2006830, BRACE2002589, BRACE2003609,
 BRACE2009318, BRACE2011677, BRACE2029396, BRACE2037299,
 BRACE2039823, BRACE2039832, BRACE2043105, BRACE3001058,
 BRACE3001113, BRACE3003026, BRACE3003053, BRACE3009127,
 BRACE3010076, BRACE3015829, BRACE3021148, BRAMY3004800,
 20 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRCOC2019841, BRHIP2005271, BRHIP3000017, BRHIP3000240,
 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 25 FEBRA2028516, HCHON2000743, IMR322001879, NT2RI2009583,
 NT2RP8000521, OCBBF2008144, OCBBF2011669, PERIC2007068,
 PUAEN2006335, SPLEN2039379, SYNOV2021953, TESTI2015626,
 TESTI4001984, TESTI4008058, TESTI4013894, TESTI4025268,
 TESTI4032090, THYMU2004284, THYMU2040925, THYMU3000360,
 30 TLIVE2002046, TRACH3000134, UTERU2008040, UTERU2011220,
 UTERU2021820, UTERU2028734

These genes are involved in equilibrium sense or motor function.

35 Genes involved in signaling from sensory organs

The thalamus is an area which comprises many neurons strongly connected to the cerebrum, and which transmits sensory information from the spinal cord or such to the responsible area of the cerebrum. The thalamus also controls the direction of movement from the cerebrum. For example, the thalamus resolves vision into the elements of size, shape, and color, and resolves sound into volume and sweetness or harshness to the ear, and then transmits this information to the sensory area of the cerebral cortex. Thus, genes whose expression levels differ between tissues of the whole brain and the thalamus are expected to be involved in signaling from sensory organs. These genes can be used to elucidate the molecular mechanism underlying signaling controlled by the brain. cDNA libraries derived from the thalamus (BRTHA) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 8). Genes whose expression levels differed between the two were the 412 clones and 56 clones listed below.

ASTRO1000009, ASTRO3000482, BLADE2008398, BRACE1000186,
 BRACE1000258, BRACE1000533, BRACE2005457, BRACE2010489,
 20 BRACE2014306, BRACE2014657, BRACE2015058, BRACE2031154,
 BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,
 BRACE3003192, BRACE3005499, BRACE3007480, BRACE3008384,
 BRACE3009237, BRACE3009724, BRACE3009747, BRACE3010397,
 BRACE3010428, BRACE3011271, BRACE3011421, BRACE3012364,
 25 BRACE3022769, BRACE3026735, BRACE3027478, BRACE3031838,
 BRALZ2011796, BRAMY2003008, BRAMY2005052, BRAMY2019300,
 BRAMY2019963, BRAMY2028914, BRAMY2031317, BRAMY2036567,
 BRAMY2037823, BRAMY2040592, BRAMY2044078, BRAMY3002803,
 BRAMY3004224, BRAMY3005091, BRAMY4000229, BRAWH1000127,
 30 BRAWH2001395, BRAWH2001671, BRAWH2001940, BRAWH2001973,
 BRAWH2002560, BRAWH2002761, BRAWH2005315, BRAWH2007658,
 BRAWH2010000, BRAWH2010084, BRAWH2010536, BRAWH2012162,
 BRAWH2012326, BRAWH2013294, BRAWH2013871, BRAWH2014414,
 BRAWH2014645, BRAWH2014662, BRAWH2014876, BRAWH2014954,
 35 BRAWH2016221, BRAWH2016439, BRAWH2016702, BRAWH2016724,
 BRAWH3000078, BRAWH3000100, BRAWH3000314, BRAWH3000491,

BRAWH3001326, BRAWH3001475, BRAWH3001891, BRAWH3002574,
BRAWH3002600, BRAWH3002819, BRAWH3002821, BRAWH3003522,
BRAWH3003555, BRAWH3003727, BRAWH3003801, BRAWH3003992,
BRAWH3004453, BRAWH3004666, BRAWH3005132, BRAWH3005422,
5 BRAWH3005912, BRAWH3005981, BRAWH3006548, BRAWH3006792,
BRAWH3007221, BRAWH3007506, BRAWH3007592, BRAWH3007726,
BRAWH3007783, BRAWH3008341, BRAWH3008697, BRAWH3008931,
BRAWH3009297, BRCAN2006297, BRCOC2003213, BRCOC2014033,
BRCOC2020142, BRHIP2000819, BRHIP2000920, BRHIP2005719,
10 BRHIP2007741, BRHIP2009474, BRHIP2013699, BRHIP2014228,
BRHIP2022221, BRHIP2024146, BRHIP3000339, BRHIP3006683,
BRHIP3007586, BRHIP3008405, BRHIP3018797, BRSSN2000684,
BRSSN2008549, BRSSN2008797, BRSSN2011738, BRSSN2014299,
BRSTN2004863, BRSTN2008052, BRSTN2015015, BRSTN2016470,
15 BRTHA1000311, BRTHA2000855, BRTHA2001462, BRTHA2002115,
BRTHA2002281, BRTHA2002376, BRTHA2002442, BRTHA2002493,
BRTHA2002608, BRTHA2002808, BRTHA2003030, BRTHA2003110,
BRTHA2003116, BRTHA2003461, BRTHA2004821, BRTHA2004978,
BRTHA2005579, BRTHA2005956, BRTHA2006075, BRTHA2006146,
20 BRTHA2006194, BRTHA2007122, BRTHA2007422, BRTHA2007603,
BRTHA2008316, BRTHA2008335, BRTHA2008527, BRTHA2008535,
BRTHA2008955, BRTHA2009311, BRTHA2009846, BRTHA2009972,
BRTHA2010073, BRTHA2010608, BRTHA2010884, BRTHA2010907,
BRTHA2011194, BRTHA2011351, BRTHA2011500, BRTHA2011641,
25 BRTHA2012392, BRTHA2012562, BRTHA2012980, BRTHA2013262,
BRTHA2013460, BRTHA2013707, BRTHA2014792, BRTHA2014828,
BRTHA2015406, BRTHA2015478, BRTHA2015696, BRTHA2015878,
BRTHA2016215, BRTHA2016496, BRTHA2016543, BRTHA2017353,
BRTHA2017985, BRTHA2018165, BRTHA2018344, BRTHA2018591,
30 BRTHA2018624, BRTHA2018707, BRTHA2019014, BRTHA2019022,
BRTHA2019048, BRTHA3000273, BRTHA3000297, BRTHA3000633,
BRTHA3001721, BRTHA3002401, BRTHA3002427, BRTHA3002933,
BRTHA3003074, BRTHA3003343, BRTHA3003449, BRTHA3003474,
BRTHA3003490, BRTHA3004475, BRTHA3005046, BRTHA3006856,
35 BRTHA3007113, BRTHA3007148, BRTHA3007319, BRTHA3007769,
BRTHA3008143, BRTHA3008310, BRTHA3008386, BRTHA3008520,

BRTHA3008778, BRTHA3009037, BRTHA3009090, BRTHA3009291,
 BRTHA3010366, BRTHA3013884, BRTHA3015815, BRTHA3015910,
 BRTHA3016845, BRTHA3016917, BRTHA3017047, BRTHA3017589,
 BRTHA3017848, BRTHA3018514, BRTHA3018617, BRTHA3018656,
 5 BRTHA3019105, COLON2001721, CTONG1000087, CTONG2008233,
 CTONG2017500, CTONG2019788, CTONG2023021, CTONG2028124,
 CTONG3000657, CTONG3001123, CTONG3008894, CTONG3009028,
 CTONG3009239, CTONG3009328, FCBBF2001183, FCBBF3001977,
 FCBBF3021576, FEBRA2007544, FEBRA2007801, FEBRA2008287,
 10 FEBRA2008360, FEBRA2020886, FEBRA2028618, HCASM2007047,
 HCHON2000028, HCHON2000212, HCHON2000244, HCHON2000626,
 HCHON2001084, HCHON2001217, HCHON2002676, HCHON2005921,
 HCHON2006250, HEART1000074, HEART2007031, HHDP1000118,
 HLUNG2001996, HLUNG2002465, IMR322000127, IMR322001380,
 15 IMR322002035, KIDNE2002252, KIDNE2005543, KIDNE2006580,
 KIDNE2011314, MESAN2006563, MESAN2012054, MESTC1000042,
 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
 NT2RI2014733, NT2RI3002842, NT2RI3002892, NT2RI3005403,
 NT2RI3006284, NT2RI3006673, NT2RI3007543, NT2RI3008055,
 20 NT2RP7004123, NT2RP7005529, NT2RP7009147, NT2RP7014005,
 NT2RP7017474, NTONG2005969, NTONG2008088, OCBBF2001794,
 OCBBF2006005, OCBBF2006764, OCBBF2007028, OCBBF2010140,
 OCBBF2020639, OCBBF2021286, OCBBF2024719, OCBBF2024850,
 OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
 25 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2002489,
 PUAEN2005930, PUAEN2006701, PUAEN2007044, PUAEN2009655,
 RECTM2001347, SKMUS2000757, SPLEN2006122, SPLEN2010912,
 SPLEN2025491, SPLEN2028914, SPLEN2031424, SPLEN2031547,
 SPLEN2032154, SPLEN2034781, SPLEN2036821, SPLEN2036932,
 30 SYNOV1000374, SYNOV2014400, SYNOV4002346, SYNOV4002883,
 SYNOV4007430, SYNOV4007671, SYNOV4008440, TESOP2002451,
 TESTI2049246, TESTI4000014, TESTI4000209, TESTI4001100,
 TESTI4002290, TESTI4006137, TESTI4008797, TESTI4009286,
 TESTI4010851, TESTI4012702, TESTI4013817, TESTI4014159,
 35 TESTI4014694, TESTI4021478, TESTI4022936, TESTI4024420,
 TESTI4027821, TESTI4037156, THYMU2001090, THYMU2025707,

THYMU2032825, THYMU2033308, THYMU2033787, THYMU2035735,
 THYMU2039315, THYMU2040975, THYMU3001234, THYMU3001379,
 THYMU3004835, THYMU3008171, TKIDN2009641, TKIDN2009889,
 TKIDN2015788, TLIVE2001327, TRACH1000205, TRACH2001549,
 5 TRACH2005811, TRACH2006049, TRACH2007834, TRACH2008300,
 TRACH2023299, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004068, TRACH3004721, TRACH3005294, TRACH3007479,
 TRACH3008093, TRACH3009455, TSTOM1000135, TUTER2000904,
 UTERU2002410, UTERU2006115, UTERU2019706, UTERU2019940,
 10 UTERU2023039, UTERU2023175, UTERU2026203, UTERU2030280,
 UTERU3000899, UTERU3001571, UTERU3001572, UTERU3004709,
 UTERU3005230, UTERU3005907, UTERU3007640, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 15 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRHIP2005271, BRHIP3000017, BRTHA2002133, BRTHA2002702,
 BRTHA2007060, BRTHA2010033, BRTHA2011321, BRTHA2013426,
 BRTHA2013610, BRTHA2016318, BRTHA2017364, BRTHA2017972,
 BRTHA2018011, BRTHA2018443, BRTHA3000296, BRTHA3003000,
 20 BRTHA3008826, CTONG2008721, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000743, HSYRA2005628, IMR322001879,
 NT2RI2009583, OCBBF2008144, PERIC2007068, PUAEN2006335,
 SPLEN2016932, SPLEN2039379, SYNOV2006620, TESTI4001984,
 25 TESTI4008058, TESTI4025268, TESTI4032090, THYMU3000360,
 TLIVE2002046, TRACH3000134, UTERU2021820, UTERU2028734

These genes are involved in signaling from sensory organs.

Genes involved in emotional reaction

30 The amygdala is the center of emotion in the brain.
 Information passing through the amygdala induces an emotional
 reaction, for example, panic or fear. When a strong fear
 reaction is produced due to the emotional evaluation of stimulus
 in the amygdala, the amygdala transmits an alert signal to each
 35 area of the brain. This results in various reactions such as
 sweating palms, palpitation, elevated blood pressure, and rapid

secretion of adrenaline. In other words, the amygdala transmits signals which cause the body to be on the alert and is a tissue involved in a kind of defense instinct. Thus, genes whose expression levels differ between tissues of the whole brain and the amygdala are expected to be involved in emotional reaction. Such genes can be used to elucidate the molecular mechanism underlying emotional reaction, fear, or panic. cDNA libraries derived from the amygdala (BRAMY) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 9). Genes whose expression levels differed between the two were the 383 clones and 55 clones listed below.

ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 BRACE1000533, BRACE2005457, BRACE2006319, BRACE2010489,
 BRACE2014657, BRACE2015058, BRACE2027258, BRACE2030341,
 15 BRACE2031389, BRACE2035381, BRACE2044286, BRACE2045954,
 BRACE3000787, BRACE3000973, BRACE3003192, BRACE3005499,
 BRACE3007480, BRACE3008036, BRACE3009237, BRACE3009724,
 BRACE3009747, BRACE3010428, BRACE3011271, BRACE3011421,
 BRACE3012364, BRACE3013780, BRACE3022769, BRACE3026735,
 20 BRACE3027478, BRACE3031838, BRALZ2011796, BRAMY2001473,
 BRAMY2003008, BRAMY2004771, BRAMY2005052, BRAMY2017528,
 BRAMY2019300, BRAMY2019963, BRAMY2019985, BRAMY2020058,
 BRAMY2020270, BRAMY2021498, BRAMY2028856, BRAMY2028914,
 BRAMY2029602, BRAMY2030098, BRAMY2030109, BRAMY2030702,
 25 BRAMY2030703, BRAMY2030799, BRAMY2031317, BRAMY2031377,
 BRAMY2031442, BRAMY2032014, BRAMY2032242, BRAMY2032317,
 BRAMY2033003, BRAMY2033116, BRAMY2033267, BRAMY2033594,
 BRAMY2034185, BRAMY2034920, BRAMY2034993, BRAMY2036387,
 BRAMY2036396, BRAMY2036567, BRAMY2036699, BRAMY2036913,
 30 BRAMY2037823, BRAMY2038100, BRAMY2038484, BRAMY2038846,
 BRAMY2038904, BRAMY2039872, BRAMY2040478, BRAMY2040592,
 BRAMY2041261, BRAMY2041378, BRAMY2041542, BRAMY2042612,
 BRAMY2042641, BRAMY2042760, BRAMY2042918, BRAMY2044078,
 BRAMY2044246, BRAMY2045036, BRAMY2046478, BRAMY2046742,
 35 BRAMY2046989, BRAMY2047169, BRAMY2047420, BRAMY2047676,
 BRAMY2047746, BRAMY2047751, BRAMY2047765, BRAMY2047884,

BRAMY3000206, BRAMY3000213, BRAMY3001401, BRAMY3001794,
 BRAMY3002312, BRAMY3002620, BRAMY3002803, BRAMY3002805,
 BRAMY3004224, BRAMY3004672, BRAMY3004900, BRAMY3004919,
 BRAMY3005091, BRAMY3005932, BRAMY3006297, BRAMY3007206,
 5 BRAMY3007609, BRAMY3008466, BRAMY3008505, BRAMY3008650,
 BRAMY3009811, BRAMY3010411, BRAMY4000095, BRAMY4000229,
 BRAMY4000277, BRAWH1000127, BRAWH2001395, BRAWH2001671,
 BRAWH2001940, BRAWH2001973, BRAWH2002560, BRAWH2002761,
 BRAWH2005315, BRAWH2007658, BRAWH2010000, BRAWH2010084,
 10 BRAWH2010536, BRAWH2012162, BRAWH2012326, BRAWH2013294,
 BRAWH2013871, BRAWH2014414, BRAWH2014645, BRAWH2014662,
 BRAWH2014876, BRAWH2014954, BRAWH2016221, BRAWH2016439,
 BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,
 BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
 15 BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
 BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
 BRAWH3003801, BRAWH3003992, BRAWH3004453, BRAWH3004666,
 BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
 BRAWH3006548, BRAWH3006792, BRAWH3007221, BRAWH3007506,
 20 BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
 BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2014881,
 BRCAN2017717, BRCOC2000670, BRCOC2003213, BRCOC2014033,
 BRCOC2020142, BRHIP2000920, BRHIP2005719, BRHIP2007741,
 BRHIP2014228, BRHIP2024146, BRHIP2026061, BRHIP3000339,
 25 BRHIP3001283, BRHIP3006683, BRHIP3007586, BRHIP3008405,
 BRHIP3018797, BRSSN2000684, BRSSN2004496, BRSSN2011738,
 BRSSN2014299, BRSTN2008052, BRSTN2010750, BRSTN2015015,
 BRSTN2016470, BRTHA1000311, BRTHA2008335, BRTHA2011641,
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 30 BRTHA3008520, BRTHA3009090, BRTHA3017848, COLON2001721,
 CTONG1000087, CTONG2008233, CTONG2017500, CTONG2028124,
 CTONG3000657, CTONG3001123, CTONG3008894, CTONG3009239,
 CTONG3009328, FCBBF2001183, FCBBF3001977, FEBRA2007544,
 FEBRA2007801, FEBRA2008287, FEBRA2010719, FEBRA2020886,
 35 FEBRA2025427, FEBRA2028618, HCASM2007047, HCHON2000244,
 HCHON2000626, HCHON2001217, HCHON2002676, HCHON2006250,

HCHON2008112, HEART1000074, HHDPC1000118, HLUNG2002465,
 HSYRA2009075, IMR322000127, IMR322001380, IMR322002035,
 KIDNE2000665, KIDNE2006580, MESAN2006563, MESAN2012054,
 MESAN2015515, MESTC1000042, NOVAR2001783, NT2NE2005890,
 5 NT2NE2006909, NT2RI2008724, NT2RI2012659, NT2RI2014733,
 NT2RI3001515, NT2RI3002892, NT2RI3005724, NT2RI3006284,
 NT2RI3006673, NT2RI3007543, NT2RI3008055, NT2RP7005529,
 NT2RP7009147, NT2RP7014005, NT2RP7017474, NTONG2005969,
 OCBBF1000254, OCBBF2001794, OCBBF2006005, OCBBF2006764,
 10 OCBBF2007028, OCBBF2007114, OCBBF2010140, OCBBF2021286,
 OCBBF2023162, OCBBF2024850, OCBBF2028935, OCBBF2035214,
 OCBBF2036743, OCBBF2038317, OCBBF3000483, OCBBF3008230,
 PEBLM2004666, PERIC2000889, PERIC2003720, PLACE6001185,
 PUAEN2005930, PUAEN2006701, PUAEN2007044, PUAEN2009174,
 15 PUAEN2009655, SKNMC2002402, SKNSH2000482, SPLEN2001599,
 SPLEN2002467, SPLEN2028914, SPLEN2029912, SPLEN2031424,
 SPLEN2031547, SPLEN2034781, SPLEN2036932, SPLEN2038345,
 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4007671, SYNOV4008440, TESOP2002451, TESTI2009474,
 20 TESTI4000014, TESTI4000209, TESTI4001100, TESTI4006137,
 TESTI4008797, TESTI4009286, TESTI4010851, TESTI4013817,
 TESTI4014159, TESTI4014694, TESTI4021478, TESTI4022936,
 TESTI4024420, TESTI4027821, TESTI4029836, TESTI4037156,
 TESTI4037188, THYMU2001090, THYMU2014353, THYMU2033308,
 25 THYMU2035735, THYMU2037226, THYMU2039315, THYMU3001234,
 THYMU3001379, THYMU3004835, THYMU3008171, TKIDN2009641,
 TKIDN2009889, TKIDN2015788, TLIVE2004320, TRACH1000205,
 TRACH2001549, TRACH2001684, TRACH2005811, TRACH2006049,
 TRACH2007834, TRACH2008300, TRACH2025344, TRACH2025535,
 30 TRACH2025911, TRACH3001427, TRACH3002192, TRACH3004068,
 TRACH3004721, TRACH3005294, TRACH3007479, TRACH3008093,
 TRACH3009455, TUTER2000904, UTERU2002410, UTERU2004929,
 UTERU2006115, UTERU2007520, UTERU2019706, UTERU2023039,
 UTERU2026203, UTERU3001572, UTERU3001766, UTERU3005230,
 35 UTERU3007640, UTERU3009517, UTERU3009871

ADRGL2000042, BLADE2006830, BRACE2003609, BRACE2039823,
 BRAMY2019111, BRAMY2035070, BRAMY2035449, BRAMY2035718,
 BRAMY2038516, BRAMY2039341, BRAMY2040159, BRAMY2041434,
 BRAMY2045471, BRAMY3004800, BRAWH1000369, BRAWH2006207,
 5 BRAWH2006395, BRAWH2008993, BRAWH2009393, BRAWH2010552,
 BRAWH3007441, BRAWH3009017, BRHIP2005271, BRHIP3000017,
 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000508, HCHON2000743, IMR322001879,
 10 NT2RI2009583, OCBBF2008144, PERIC2007068, PUAEN2006335,
 SPLEN2039379, TESTI2015626, TESTI2026647, TESTI4001984,
 TESTI4008058, TESTI4013894, TESTI4025268, TESTI4032090,
 THYMU3000360, TKIDN2018926, TLIVE2002046, TRACH3000134,
 UTERU2008040, UTERU2021820, UTERU2028734

15 These genes are involved in emotional reaction.

Cancer-related genes

Cancer tissues are assumed to express a distinct set of
 genes distinct from normal tissues, and thus expression of these
 20 genes can contribute to carcinogenesis in tissues and cells.
 Thus, genes whose expression patterns in cancer tissues differ
 from those in normal tissues are cancer-related genes. A search
 was carried out for genes whose expression levels in cancer
 tissues differed from those in normal tissues.

25 The result of comparative analysis of cDNA libraries
 derived from breast tumor (TBAES) and normal breast (BEAST)
 (Table 10) showed that the genes whose expression levels
 differed between the two were the 35 and four clones listed
 below.

30 ASTRO2002842, BRACE3016884, BRSSN2011262, BRTHA2008335,
 HCHON2000244, HCHON2006250, HEART1000010, MESAN2012054,
 NT2RP7000466, NT2RP7009147, OCBBF2021020, PEBLM2002749,
 PEBLM2004666, SPLEN2001599, SPLEN2031547, STOMA1000189,
 TBAES2001171, TBAES2001220, TBAES2001229, TBAES2001258,
 35 TBAES2001492, TBAES2001751, TBAES2002197, TBAES2003550,
 TBAES2004055, TBAES2005157, TBAES2005543, TBAES2006568,

TBAES2007964, TESTI4000014, TESTI4037156, TRACH3002192,
 TRACH3004068, TSTOM2000553, UTERU2002410
 BRAWH2006395, NT2RI2009583, STOMA2004893, TBAES2000932

The result of comparative analysis of cDNA libraries
 5 derived from cervical tumor (TCERX) and normal cervical duct
 (CERVX) (Table 11) showed that the genes whose expression levels
 differed between the two were twelve and two clones listed below.
 BLADE2007666, BRAMY2047420, BRCAN2007409, BRSTN2016470,
 CERVX1000042, CERVX2002006, MESAN2006563, PROST2018090,
 10 TCERX2000613, TESTI4037156, THYMU2031341, UTERU2004688
 CERVX2002013, NT2RI2009583

The result of comparative analysis of cDNA libraries
 derived from colon tumor (TCOLN) and normal colon (COLON) (Table
 12) showed that the genes whose expression levels differed
 15 between the two were the 24 and four clones listed below.
 BRACE3015027, BRAMY2040592, BRSTN2016470, COLON1000030,
 COLON2000470, COLON2000568, COLON2001721, COLON2002443,
 COLON2002520, COLON2003043, COLON2004478, COLON2005126,
 COLON2005772, COLON2006282, COLON2009499, OCBBF2028935,
 20 PLACE7000514, RECTM2000433, SYNOV4007671, TCOLN2002278,
 TESTI2052693, TESTI4037156, THYMU2031368, TRACH2025535
 CTONG1000113, NT2RI2009583, NT2RI2018448, TESTI2015626

The result of comparative analysis of cDNA libraries
 derived from esophageal tumor (TESOP) and normal esophagus
 25 (NESOP) (Table 13) showed that the genes whose expression levels
 differed between the two were the 56 and ten clones listed below.
 BRACE2030341, BRAMY2047420, BRHIP2003917, BRTHA2003461,
 CTONG2013178, D3OST3000169, FEBRA2025427, HCHON2000244,
 HHDPC1000118, NESOP2000744, NESOP2001433, NESOP2001656,
 30 NESOP2001694, NESOP2001752, NESOP2002738, NT2RI3006284,
 NT2RP7009147, PLACE6019932, SYNOV2005216, TESOP1000127,
 TESOP2000801, TESOP2001122, TESOP2001166, TESOP2001345,
 TESOP2001605, TESOP2001818, TESOP2001849, TESOP2001865,
 TESOP2001953, TESOP2002273, TESOP2002451, TESOP2002489,
 35 TESOP2002539, TESOP2002950, TESOP2003273, TESOP2003753,
 TESOP2004114, TESOP2005285, TESOP2005485, TESOP2005579,

TESOP2006041, TESOP2006060, TESOP2006068, TESOP2006670,
 TESOP2006746, TESOP2007052, TESOP2007262, TESOP2007636,
 TESOP2007688, TESOP2009121, TESOP2009555, TESTI4009286,
 TESTI4010851, THYMU2040975, TRACH2005811, UTERU2023175
 5 CTONG2016942, NT2RI2009583, TESOP2000390, TESOP2001796,
 TESOP2005199, TESOP2006398, TESOP2006865, TESOP2007384,
 TESTI2015626, TRACH2000862

The result of comparative analysis of cDNA libraries
 derived from kidney tumor (TKIDN) and normal kidney (KIDNE)
 10 (Table 14) showed that the genes whose expression levels
 differed between the two were the 96 and 13 clones listed below.
 ASTRO2018373, BRACE1000186, BRACE2014306, BRACE2015058,
 BRACE2016981, BRACE2043665, BRACE3008036, BRACE3010428,
 BRACE3022769, BRAMY2019963, BRAMY2044078, BRAWH1000127,
 15 BRAWH2001395, BRAWH2001671, BRAWH2013294, BRAWH2014645,
 BRHIP2024146, BRHIP3000339, BRSSN2000684, BRSSN2004719,
 BRSSN2018581, BRSTN2016470, BRTHA1000311, BRTHA3002427,
 CTONG1000087, CTONG2028124, CTONG3000657, CTONG3008894,
 FCBBF2001183, FEBRA2008287, HCASM2001301, HCHON2000028,
 20 HCHON2000244, HEART1000074, HHDPC1000118, HSYRA2008376,
 KIDNE1000064, KIDNE2000665, KIDNE2000722, KIDNE2000832,
 KIDNE2000846, KIDNE2001361, KIDNE2001847, KIDNE2002252,
 KIDNE2002991, KIDNE2003837, KIDNE2005543, KIDNE2006580,
 KIDNE2010264, KIDNE2011314, KIDNE2011532, KIDNE2011635,
 25 KIDNE2012945, KIDNE2013095, NESOP2001656, NTONG2005969,
 PEBLM2004666, SKMUS2000757, STOMA1000189, SYNOV4007671,
 TBAES2001258, TESTI4000014, TESTI4001100, TESTI4012702,
 TESTI4046819, THYMU2032014, TKIDN2000701, TKIDN2002424,
 TKIDN2002632, TKIDN2003044, TKIDN2004386, TKIDN2005934,
 30 TKIDN2005947, TKIDN2006525, TKIDN2006852, TKIDN2007667,
 TKIDN2009092, TKIDN2009641, TKIDN2009889, TKIDN2010934,
 TKIDN2012824, TKIDN2013287, TKIDN2014757, TKIDN2014771,
 TKIDN2015263, TKIDN2015788, TKIDN2016309, TKIDN2019116,
 TRACH2001443, TRACH2001684, TRACH2007834, TRACH2008300,
 35 TRACH3001427, UTERU2002410, UTERU2023175, UTERU3001572

BLADE2006830, BRALZ2017844, CTONG2028758, FCBBF1000509,
 FEBRA2001990, FEBRA2028516, HCHON2000508, MESAN2005303,
 NT2RI2009583, TESTI2015626, TKIDN2008778, TKIDN2012771,
 TKIDN2018926

5 The result of comparative analysis of cDNA libraries
 derived from liver tumor (TLIVE) and normal liver (LIVER) (Table
 15) showed that the genes whose expression levels differed
 between the two were the 35 and six clones listed below.
 BRCAN2018935, BRSTN2016470, BRTHA2012980, BRTHA3002427,
 10 CTONG2028124, LIVER2007415, NT2RI2008724, SPLEN2012624,
 SPLEN2033098, TESOP2002451, TLIVE2000023, TLIVE2001327,
 TLIVE2001828, TLIVE2001927, TLIVE2002336, TLIVE2002338,
 TLIVE2002690, TLIVE2003197, TLIVE2003225, TLIVE2003381,
 TLIVE2003970, TLIVE2004110, TLIVE2004320, TLIVE2004601,
 15 TLIVE2005180, TLIVE2006236, TLIVE2006529, TLIVE2007132,
 TLIVE2007528, TLIVE2007816, TLIVE2008083, TLIVE2008229,
 TLIVE2009541, UTERU2002410, UTERU2005621
 LIVER2000247, NT2RI2009583, TESTI2015626, TLIVE2001684,
 TLIVE2002046, TLIVE2007607

20 The result of comparative analysis of cDNA libraries
 derived from lung tumor (TLUNG) and normal lung (HLUNG) (Table
 16) showed that the genes whose expression levels differed
 between the two were the 47 and nine clones listed below.
 BRCAN2021028, BRHIP2000819, BRSTN2016470, CTONG1000087,
 25 CTONG2028124, HCHON2006250, HEART1000074, HLUNG1000017,
 HLUNG2000014, HLUNG2001996, HLUNG2002465, HLUNG2002958,
 HLUNG2003003, HLUNG2003872, HLUNG2010464, HLUNG2011041,
 HLUNG2011298, HLUNG2012049, HLUNG2012287, HLUNG2012727,
 HLUNG2013204, HLUNG2013304, HLUNG2013622, HLUNG2013851,
 30 HLUNG2014262, HLUNG2014288, HLUNG2014449, HLUNG2015617,
 HLUNG2017350, HLUNG2017546, HLUNG2017806, HLUNG2019058,
 HSYRA2008376, KIDNE2012945, NT2RI2003993, NT2RP7013795,
 OCBBF3000483, SPLEN2028914, SPLEN2031547, SYNOV4007671,
 TESOP1000127, TESTI2003573, TESTI4000014, TESTI4037156,
 35 TRACH2005811, TRACH3004068, UTERU2005621

FEBRA2028516, HCHON2000508, HLUNG2013350, HLUNG2015418,
 HLUNG2015548, HLUNG2016862, NT2RI2009583, TESTI2015626,
 TRACH2019672

The result of comparative analysis of cDNA libraries
 5 derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table
 17A) showed the genes whose expression levels differed between
 the two were the 16 clones listed below.

CTONG2019788, FEBRA2014213, HLUNG2017546, NOVAR2000136,
 NOVAR2000710, NOVAR2000962, NOVAR2001108, NOVAR2001783,
 10 OCBBF3007516, TESTI2052693, TOVAR2000649, TOVAR2001281,
 TOVAR2001730, TOVAR2002247, TOVAR2002549, TRACH3004068

The result of comparative analysis of cDNA libraries
 derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table
 17B) showed the gene whose expression level was different
 15 between the two was the one clone described below. There was no
 difference in expression levels of this gene between normal and
 diseased ovaries, however there was a significant difference in
 the expression level in both tumorous and normal ovaries when
 compared with in other tissues. Thus, this gene is an ovary-
 20 specific gene and can be used as a diagnostic marker due to its
 association with disease.

TESTI2015626

The result of comparative analysis of cDNA libraries
 derived from stomach tumor (TSTOM) and normal stomach (STOMA)
 25 (Table 18) showed that the genes whose expression levels
 differed between the two were the 31 and five clones listed
 below.

BRACE2024627, BRAWH2014645, BRCAN2028355, BRHIP2000819,
 BRSTN2016470, BRTHA3003490, COLON2002443, HEART1000010,
 30 HLUNG2002465, KIDNE2001847, NT2RP7000466, PUAEN2006328,
 SMINT2001818, STOMA1000189, STOMA2003444, STOMA2004294,
 STOMA2004925, STOMA2008546, SYNOV4007671, TESTI4000014,
 TESTI4010851, THYMU2035735, TRACH2001549, TRACH2005811,
 TRACH2025535, TSTOM1000135, TSTOM2000442, TSTOM2000553,
 35 TSTOM2002672, UTERU2006115, UTERU3001572

FEBRA2008692, NT2RI2009583, STOMA2003158, STOMA2004893,
TESTI2015626

The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) (Table 19) showed that the genes whose expression levels differed between the two were the 244 and 34 clones listed below.

5 BNGH42007788, BRACE1000186, BRACE2030341, BRACE3008772,
BRACE3009747, BRACE3010428, BRACE3027478, BRALZ2017359,
BRAWH2014645, BRAWH3000314, BRAWH3001326, BRAWH3002574,
10 BRAWH3002821, BRAWH3003727, BRAWH3007592, BRCAN2009432,
BRCAN2028355, BRHIP3007586, BRHIP3008344, BRHIP3008565,
BRSSN2006892, BRSTN2001067, BRSTN2016470, BRTHA2010608,
BRTHA3003074, CTONG1000087, CTONG1000467, CTONG2028124,
CTONG3001123, CTONG3008894, CTONG3009028, CTONG3009239,
15 FCBBF3004847, FEBRA2026984, FEBRA2028618, HCHON2000244,
HCHON2000418, HCHON2000626, HCHON2001084, HCHON2001217,
HCHON2005921, HCHON2006250, HCHON2008444, HLUNG2003003,
HSYRA2008376, KIDNE2002252, MESAN2014295, NOVAR2000710,
NT2RI2008724, NT2RI2014247, NT2RI2014733, NT2RI3002892,
20 NT2RI3005724, NT2RI3006284, NT2RI3006340, NT2RI3006673,
NT2RI3007291, NT2RI3007543, NT2RP7004123, NT2RP7005529,
NT2RP7009147, NT2RP7017474, OCBBF2007028, OCBBF2020741,
OCBBF2024850, OCBBF2036743, OCBBF3000483, PLACE6001185,
PLACE7000514, PUAEN2007044, PUAEN2009655, SKNSH2000482,
25 SPLEN2006122, SPLEN2016554, SPLEN2031547, SPLEN2036932,
STOMA1000189, STOMA2004925, SYNOV2017055, SYNOV4001395,
SYNOV4002346, SYNOV4008440, TCERX2000613, TESOP2002273,
TESTI4000014, TESTI4008797, TESTI4009286, TESTI4012702,
TESTI4013675, TESTI4014159, TESTI4018886, TESTI4029671,
30 TESTI4037156, THYMU2008725, THYMU2031890, THYMU2033070,
THYMU2035735, THYMU3001472, TRACH1000205, TRACH2001443,
TRACH2001549, TRACH2005811, TRACH2007834, TRACH2008300,
TRACH3002192, TRACH3003379, TRACH3004068, TRACH3004721,
TRACH3007479, TUTER1000122, TUTER2000425, TUTER2000904,
35 TUTER2000916, TUTER2001387, TUTER2002729, UTERU1000024,
UTERU1000031, UTERU1000148, UTERU1000249, UTERU1000337,

UTERU1000339, UTERU2000649, UTERU2001409, UTERU2002410,
UTERU2002841, UTERU2004688, UTERU2004929, UTERU2005004,
UTERU2005621, UTERU2006115, UTERU2006137, UTERU2006568,
UTERU2007444, UTERU2007520, UTERU2007724, UTERU2008347,
5 UTERU2014678, UTERU2017762, UTERU2019491, UTERU2019681,
UTERU2019706, UTERU2019940, UTERU2020491, UTERU2020718,
UTERU2021163, UTERU2021380, UTERU2022020, UTERU2022981,
UTERU2023039, UTERU2023175, UTERU2023651, UTERU2023712,
UTERU2024002, UTERU2024656, UTERU2025025, UTERU2025645,
10 UTERU2025891, UTERU2026025, UTERU2026090, UTERU2026203,
UTERU2027591, UTERU2029953, UTERU2030213, UTERU2030280,
UTERU2031084, UTERU2031268, UTERU2031521, UTERU2031703,
UTERU2031851, UTERU2033375, UTERU2033382, UTERU2035114,
UTERU2035323, UTERU2035328, UTERU2035331, UTERU2035452,
15 UTERU2035469, UTERU2035503, UTERU2035745, UTERU2036089,
UTERU2037361, UTERU2037577, UTERU2038251, UTERU3000226,
UTERU3000645, UTERU3000665, UTERU3000828, UTERU3000899,
UTERU3001059, UTERU3001240, UTERU3001542, UTERU3001571,
UTERU3001572, UTERU3001585, UTERU3001652, UTERU3001766,
20 UTERU3001988, UTERU3002209, UTERU3002218, UTERU3002383,
UTERU3002667, UTERU3002731, UTERU3002768, UTERU3002786,
UTERU3002993, UTERU3003116, UTERU3003135, UTERU3003178,
UTERU3003465, UTERU3003523, UTERU3003776, UTERU3004523,
UTERU3004616, UTERU3004709, UTERU3004992, UTERU3005049,
25 UTERU3005205, UTERU3005230, UTERU3005460, UTERU3005585,
UTERU3005907, UTERU3005970, UTERU3006008, UTERU3006308,
UTERU3007134, UTERU3007419, UTERU3007640, UTERU3007913,
UTERU3008660, UTERU3008671, UTERU3009259, UTERU3009490,
UTERU3009517, UTERU3009690, UTERU3009871, UTERU3009979,
30 UTERU3011063, UTERU3015086, UTERU3015500, UTERU3016789,
UTERU3018081, UTERU3018154, UTERU3018616, UTERU3018711
ADRGL2000042, BRHIP3000017, CTONG2003348, CTONG2019822,
CTONG2020378, CTONG2020411, CTONG2024031, FEBRA2028516,
HCASM2008536, HCHON2000743, IMR322001879, MESAN2005303,
35 NT2RI2009583, OCBBF2008144, PERIC2007068, SPLEN2039379,
TESTI2015626, TESTI4013894, TUTER2000057, UTERU2004299,

UTERU2008040, UTERU2011220, UTERU2019534, UTERU2021820,
 UTERU2028734, UTERU2032279, UTERU2033577, UTERU2035978,
 UTERU3000402, UTERU3000738, UTERU3001053, UTERU3014791,
 UTERU3015412, UTERU3017176

5 The result of comparative analysis of cDNA libraries
 derived from tongue cancer (CTONG) and normal tongue (NTONG)
 (Table 20) showed that the genes whose expression levels
 differed between the two were the 166 and 31 clones listed below.

10 BNGH42007788, BRACE1000186, BRACE2006319, BRACE3010428,
 BRACE3012364, BRAMY2020058, BRAMY3002803, BRAWH2001671,
 BRAWH2014645, BRAWH3002574, BRCAN2009432, BRCAN2015371,
 BRCAN2020710, BRHIP2004814, BRHIP3018797, BRTHA2003461,
 BRTHA3003490, CTONG1000087, CTONG1000088, CTONG1000288,
 CTONG1000302, CTONG1000341, CTONG1000467, CTONG1000488,
 15 CTONG1000508, CTONG1000540, CTONG2000042, CTONG2001877,
 CTONG2004062, CTONG2006798, CTONG2008233, CTONG2009423,
 CTONG2009531, CTONG2010803, CTONG2013178, CTONG2017500,
 CTONG2019248, CTONG2019652, CTONG2019704, CTONG2019788,
 CTONG2019833, CTONG2020127, CTONG2020522, CTONG2020638,
 20 CTONG2020806, CTONG2021132, CTONG2022153, CTONG2022601,
 CTONG2023021, CTONG2023512, CTONG2024206, CTONG2024749,
 CTONG2025496, CTONG2025516, CTONG2025900, CTONG2026920,
 CTONG2027327, CTONG2028124, CTONG2028687, CTONG3000084,
 CTONG3000657, CTONG3000686, CTONG3000707, CTONG3000896,
 25 CTONG3001123, CTONG3001370, CTONG3001420, CTONG3001560,
 CTONG3002020, CTONG3002127, CTONG3002412, CTONG3002674,
 CTONG3003179, CTONG3003483, CTONG3003652, CTONG3003654,
 CTONG3003737, CTONG3003905, CTONG3003972, CTONG3004072,
 CTONG3004712, CTONG3005325, CTONG3005648, CTONG3005713,
 30 CTONG3005813, CTONG3006067, CTONG3006186, CTONG3006650,
 CTONG3007444, CTONG3007528, CTONG3007586, CTONG3007870,
 CTONG3008252, CTONG3008258, CTONG3008496, CTONG3008566,
 CTONG3008639, CTONG3008831, CTONG3008894, CTONG3008951,
 CTONG3009028, CTONG3009227, CTONG3009239, CTONG3009328,
 35 CTONG3009385, FEBRA2007544, FEBRA2007801, FEBRA2021966,
 FEBRA2025427, HCHON2000028, HCHON2001217, HHDPC1000118,

HSYRA2008376, KIDNE2001847, KIDNE2002252, MESAN2006563,
 NT2RI2008724, NT2RI2018883, NT2RI3000622, NT2RI3006284,
 NT2RI3006673, NT2RI3007543, NT2RI3007757, NT2RP7004123,
 NT2RP7009147, NT2RP7014005, NTONG2000413, NTONG2003852,
 5 NTONG2005277, NTONG2005969, NTONG2006354, NTONG2007249,
 NTONG2007517, NTONG2008088, NTONG2008672, OCBBF2001794,
 OCBBF2006151, PEBLM2004666, PEBLM2005183, SPLEN2002467,
 SPLEN2029912, SPLEN2031547, SYNOV4007671, SYNOV4008440,
 TBAES2002197, TESOP2002273, TESTI2009474, TESTI4000014,
 10 TESTI4000209, TESTI4008018, TESTI4009286, TESTI4010851,
 TESTI4012702, TESTI4013675, THYMU2031847, THYMU2033308,
 TLIVE2002690, TRACH2005811, TRACH2007059, TRACH2025535,
 TRACH3001427, TSTOM2000553, UTERU2005621, UTERU2017762,
 UTERU2023175, UTERU3001572
 15 BLADE2006830, BRHIP3000017, CTONG1000113, CTONG2003348,
 CTONG2004000, CTONG2008721, CTONG2015596, CTONG2015633,
 CTONG2016942, CTONG2019822, CTONG2020374, CTONG2020378,
 CTONG2020411, CTONG2020974, CTONG2024031, CTONG2028758,
 CTONG3001501, CTONG3002552, CTONG3003598, CTONG3004550,
 20 CTONG3004726, CTONG3009287, FEBRA2008692, FEBRA2028516,
 HCHON2000508, NT2RI2009583, NTONG2008093, PERIC2007068,
 TESOP2007384, TLIVE2002046, TRACH2000862

These genes are involved in cancer.

Expression frequency analysis is used when searching for
 25 genes involved in development and differentiation, where the
 expression levels of genes in developing and/or differentiating
 tissues and/or cells are compared with those in adult tissues
 and/or cells. Genes involved in tissue development and/or
 differentiation are genes which participate in tissue
 30 construction and function expression. These genes are thus
 useful genes available for medicine aiming at regeneration of
 injured tissues.

By using information on gene expression frequency gained
 from the database of the nucleotide sequences of the 1,402,069
 35 clones as described above, genes whose expression frequencies

differed between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, were analyzed.

The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain
 5 (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) (Table 21) showed that the genes whose expression levels differed between the two were the 1,035 and 139 clones listed below.

ADRGL2009146, ADRGL2012038, ADRGL2012179, ASTRO1000009,
 10 ASTRO2003960, ASTRO3000482, BLADE1000176, BLADE2001371,
 BLADE2004089, BLADE2008398, BNGH42007788, BRACE1000186,
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 15 BRACE2015058, BRACE2015314, BRACE2016981, BRACE2018762,
 BRACE2024627, BRACE2026836, BRACE2027258, BRACE2027970,
 BRACE2028970, BRACE2029112, BRACE2029849, BRACE2030326,
 BRACE2030341, BRACE2030884, BRACE2031154, BRACE2031389,
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 20 BRACE2032329, BRACE2032385, BRACE2032538, BRACE2032823,
 BRACE2033720, BRACE2035381, BRACE2035441, BRACE2036005,
 BRACE2036096, BRACE2036830, BRACE2036834, BRACE2037847,
 BRACE2038114, BRACE2038329, BRACE2038551, BRACE2039249,
 BRACE2039327, BRACE2039475, BRACE2039734, BRACE2040138,
 25 BRACE2040325, BRACE2041009, BRACE2041200, BRACE2041264,
 BRACE2042550, BRACE2043142, BRACE2043248, BRACE2043349,
 BRACE2043665, BRACE2044286, BRACE2044816, BRACE2044949,
 BRACE2045300, BRACE2045428, BRACE2045596, BRACE2045772,
 BRACE2045947, BRACE2045954, BRACE2046251, BRACE2046295,
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 BRACE3004358, BRACE3004435, BRACE3004772, BRACE3004783,

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10 PUAEN2009174, PUAEN2009655, RECTM2001347, SKMUS2000757,
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 BRTHA2010033, BRTHA2011321, BRTHA2013426, BRTHA2013610,
 BRTHA2016318, BRTHA2017364, BRTHA2017972, BRTHA2018011,
 BRTHA2018443, BRTHA3000296, BRTHA3003000, BRTHA3008826,
 CTONG2008721, CTONG2020374, CTONG2020378, CTONG2020411,
 35 CTONG2024031, CTONG3004726, FCBBF1000509, FCBBF3010361,
 FCBBF3027854, FEBRA2000790, FEBRA2001990, FEBRA2006519,

FEBRA2008692, FEBRA2014122, FEBRA2027609, FEBRA2028516,
 HCASM2003018, HCHON2000508, HCHON2000743, HCHON2004858,
 HSYRA2005628, IMR322001879, NT2RI2009583, NT2RP8000521,
 OCBBF2003327, OCBBF2005433, OCBBF2006987, OCBBF2008144,
 5 OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2020048,
 OCBBF2030116, OCBBF2032274, OCBBF2034637, OCBBF3002654,
 OCBBF3003761, OCBBF3004972, PERIC2007068, PUAEN2006335,
 SPLEN2016932, SPLEN2039379, SYNOV2006620, SYNOV2021953,
 TESTI1000266, TESTI2015626, TESTI2026647, TESTI4000214,
 10 TESTI4001984, TESTI4008058, TESTI4013894, TESTI4015442,
 TESTI4017714, TESTI4025268, TESTI4025547, TESTI4026207,
 TESTI4032090, THYMU2004284, THYMU2040925, THYMU3000360,
 TKIDN2018926, TLIVE2002046, TRACH3000134, UTERU2008040,
 UTERU2011220, UTERU2021820, UTERU2028734

15 The result of comparative analysis of cDNA libraries
 derived from fetal heart (FEHRT) and adult heart (HEART) (Table
 22) showed that the genes whose expression levels differed
 between the two were the 34 and two clones listed below.

BRAMY2040592, BRAWH2001671, BRSTN2016470, CTONG2017500,
 20 CTONG2028124, CTONG3000657, D3OST3000169, FEBRA2008287,
 HCHON2000244, HCHON2000626, HEART1000010, HEART1000074,
 HEART1000088, HEART1000139, HEART2001680, HEART2001756,
 HEART2006131, HEART2006909, HEART2007031, HEART2010391,
 HEART2010492, HEART2010495, KIDNE2000665, NB9N41000340,
 25 NT2RI2003993, NT2RI3002892, OCBBF2024850, SKMUS2006394,
 SMINT2001818, TESTI4000209, TKIDN2015788, TRACH3002192,
 TRACH3005294, TRACH3007479
 HEART2009680, THYMU2004284

30 The result of comparative analysis of cDNA libraries
 derived from fetal kidney (FEKID) and adult kidney (KIDNE)
 (Table 23) showed that the genes whose expression levels
 differed between the two were the 40 and two clones listed below.

BRACE2043665, BRACE3010428, BRSTN2016470, CTONG1000087,
 CTONG2028124, CTONG3008894, HCASM2003415, HCHON2000244,
 35 HEART1000074, HHDPC1000118, KIDNE1000064, KIDNE2000665,
 KIDNE2000722, KIDNE2000832, KIDNE2000846, KIDNE2001361,

KIDNE2001847, KIDNE2002252, KIDNE2002991, KIDNE2003837,
 KIDNE2005543, KIDNE2006580, KIDNE2010264, KIDNE2011314,
 KIDNE2011532, KIDNE2011635, KIDNE2012945, KIDNE2013095,
 PEBLM2004666, PLACE6019385, STOMA1000189, SYNOV4007671,
 5 TBAES2001258, TESOP2002451, TESTI4000014, TESTI4012702,
 THYMU2032014, TRACH2001684, TRACH2007834, UTERU2023175
 NT2RI2009583, OCBBF2008144

The result of comparative analysis of cDNA libraries
 derived from fetal lung (FELNG) and adult lung (HLUNG) (Table
 10 24) showed that the genes whose expression levels differed
 between the two were the 51 and eight clones listed below.

BRAWH3007592, BRCAN2021028, BRHIP2000819, BRSTN2016470,
 CTONG1000087, CTONG2028124, HCASM2007047, HEART1000074,
 HLUNG1000017, HLUNG2000014, HLUNG2001996, HLUNG2002465,
 15 HLUNG2002958, HLUNG2003003, HLUNG2003872, HLUNG2010464,
 HLUNG2011041, HLUNG2011298, HLUNG2012049, HLUNG2012287,
 HLUNG2012727, HLUNG2013204, HLUNG2013304, HLUNG2013622,
 HLUNG2013851, HLUNG2014262, HLUNG2014288, HLUNG2014449,
 HLUNG2015617, HLUNG2017350, HLUNG2017546, HLUNG2017806,
 20 HLUNG2019058, HSYRA2008376, KIDNE2012945, NT2RI2003993,
 NT2RI3007543, OCBBF3000483, SMINT1000192, SPLEN2028914,
 SPLEN2031547, STOMA1000189, SYNOV4007671, TESOP1000127,
 TESTI2003573, TESTI4000014, TESTI4037156, TRACH2005811,
 TRACH3004068, UTERU2005621, UTERU2023175
 25 FEBRA2028516, HCHON2000508, HLUNG2013350, HLUNG2015418,
 HLUNG2015548, HLUNG2016862, TESTI2015626, TRACH2019672

These genes are involved in regeneration of tissues and/or
 cells.

For example, if a polypeptide encoded by a cDNA of the
 30 present invention is a regulatory factor for cellular conditions
 such as growth and differentiation, it can be used for
 developing medicines as follows. The polypeptide or antibody
 provided by the present invention is injected into cells using
 microinjection, and then low molecular weight compounds and such
 35 can be screened by using, as an index, change in cellular
 conditions (such as growth and differentiation), or

activation/inhibition of a particular gene in the cell. The screening can be performed as follows.

A polypeptide of the present invention is first expressed and purified as a recombinant. This purified polypeptide is then microinjected into cells such as various cell lines, or primary culture cells, and cellular changes such as growth and differentiation are examined. Alternatively, induction of a gene whose expression is known to be involved in the change of a particular cellular condition may be detected using mRNA or polypeptide amounts. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) may be detected, where that amount is changed by the function of a gene product (polypeptide) known to influence change in a particular cellular condition. The compounds to be screened (including both low and high molecular compounds) can be added to culture media and screened using, as an index, their ability to change a cellular condition.

Cell lines introduced with a gene of the present invention can be used for screening, even without microinjection. If the product of a gene of the present invention is revealed to be involved in a particular change in cellular conditions, the change in that product can be used as an index for screening. Once a compound which can activate or inhibit the function of a polypeptide of the present invention has been developed using this screening, such a compound can be practically applied in medicines.

If a polypeptide encoded by a cDNA of the present invention is a secretory or membrane protein, or a protein involved in signal transduction, glycoproteins, transcription, or disease, it can be used in functional assays for developing medicines as described below.

In case of a membrane protein, the polypeptide is very likely to function as a receptor or ligand on the cell surface. Therefore, it is possible to reveal new ligand-receptor relationships by screening membrane proteins of the present invention, based on binding activity with known or new ligands

or receptors. Screening can be performed according to known methods.

For example, a ligand against a polypeptide of the present invention can be screened in the following manner. Namely, a
5 ligand that binds to a specific polypeptide can be screened using a method comprising the steps of: (a) contacting a test sample with a polypeptide of the present invention, or partial peptide thereof, or cells expressing such, and (b) selecting a test sample that binds to said polypeptide, said partial peptide,
10 or said cells.

Screening using cells expressing receptor polypeptides of the present invention can also be performed, for example, as follows. Receptors capable of binding to a specific polypeptide can be screened by (a) attaching sample cells to a polypeptide
15 of the present invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

For example, screening can be carried out as follows: a polypeptide of the present invention is first expressed, the
20 recombinant polypeptide is purified and labeled, a binding assay is performed using various cell lines or primary cultured cells, and cells that express the receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu
25 edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the present invention can be labeled with RI such as ^{125}I , and enzyme (alkaline phosphatase etc.).

Alternatively, a polypeptide of the present invention may be used without labeling and then detected by using a labeled
30 antibody against that polypeptide. Cells expressing a receptor polypeptide of the present invention, and selected using the above screening methods, can be applied as mentioned below to screen agonists or antagonists of that receptor.

Once a ligand binding to a polypeptide of the present
35 invention, a receptor of that polypeptide, or cells expressing that receptor have been obtained by screening as described above,

a compound binding to that ligand or receptor can be screened. It is also possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by using this binding activity as an index.

5 When a polypeptide of the present invention is a receptor, the screening method comprises the steps of (a) contacting the ligand with a polypeptide of the present invention, or cells expressing that polypeptide, in the presence of a test sample, (b) detecting binding activity between that polypeptide or cells
10 expressing that polypeptide and the ligand, and (c) selecting a compound that can reduce that binding activity when compared to activity in the absence of the test sample. Furthermore, when a polypeptide of the present invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of
15 the present invention with its receptor or cells expressing that receptor, in the presence of a test sample, (b) detecting binding activity between the polypeptide and its receptor, or cells expressing that receptor, and (c) selecting a compound that can reduce that binding activity compared to activity in
20 the absence of the test sample.

 Examples of test samples to screen include, but are not limited to, cell extracts, expressed gene library products, synthesized low molecular compounds, synthesized peptides, and natural compounds. A compound that is isolated by the above
25 screening can also be used as a test sample, using binding activity with a polypeptide of the present invention as an index.

 A compound isolated using this screening may be a candidate agonist or antagonist of a polypeptide or polypeptide receptor of the present invention. By monitoring changes in
30 intracellular signals, such as phosphorylation due to reduced binding between a polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the polypeptide receptor of the present invention. Also, the screened compound may be a candidate for a compound
35 that can inhibit interaction between a polypeptide and its associated molecules (including receptors) *in vivo*. The

polypeptides of this invention, receptors that bind to those polypeptides or ligands, and compounds thereof, can be applied in the development of preventative, therapeutic or testing agents for diseases in which the polypeptides of the present invention are involved.

Secretory proteins may regulate cellular conditions such as growth and differentiation. A novel factor that regulates cellular conditions can be found by i) adding a secretory protein of the present invention to a certain kind of cell, and ii) screening using as an index cellular changes in growth or differentiation, or activation of a particular gene.

Screening can be performed, for example, as follows. First, a polypeptide of the present invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to various cell lines or primary cultured cells, and changes in cell growth and differentiation are monitored. The induction of a particular gene known to be involved in a certain cellular change is detected using mRNA and polypeptide amounts. Alternatively, detection can be carried out using the amount of an intracellular molecule (low-molecular-weight compounds, etc.) changed by the action of a gene product (polypeptide) which influences a certain cellular change.

If screening reveals that a polypeptide of the present invention can regulate cellular conditions or functions, it is possible to apply that polypeptide as a pharmaceutical and diagnostic medicine for related diseases, either directly or by altering a part of it into an appropriate composition.

As for membrane proteins as described above, a secretory protein provided by the present invention may be used to explore a novel ligand-receptor interaction by screening based on binding activity to a known or new ligand or receptor. A similar method can be used to identify an agonist or antagonist. Compounds obtained by these methods are candidate compounds for inhibiting the interaction between the polypeptide of the present invention and an interacting molecule (including receptors). These compounds may be applied as preventive,

therapeutic, or testing agents for diseases in which the polypeptide plays a role.

Proteins involved in signal transduction or transcription may be factors that affect a certain polypeptide or gene in response to intra- or extra-cellular stimuli. A novel factor able to affect a polypeptide or gene can be found by expressing a polypeptide provided by the present invention in a certain type of cell, and screening using as an index the activation of a certain intracellular polypeptide or gene.

Screening may be performed as follows. First, a transformed cell line which expresses a polypeptide of the present invention is obtained. Then, changes in a certain gene between the transformed and the original untransformed cell lines are detected using mRNA or polypeptide amounts. Alternatively, detection may be carried out using the amount of an intracellular molecule (low molecular weight compounds, etc.) changed by the function of a certain gene product (polypeptide). Furthermore, change in expression of a certain gene can be detected by estimating the activity of a marker gene product (polypeptide), where the polypeptide of the present invention is expressed in a cell that has been introduced with a fusion gene comprising a regulatory region of the certain gene and a marker gene (luciferase, β -galactosidase, etc.).

If the polypeptide or gene influenced by a protein of the present invention is involved in disease, it is possible to screen a gene or compound that can regulate that polypeptide or gene's expression and/or activity, either directly or indirectly, by utilizing a polypeptide of the present invention.

For example, a polypeptide of the present invention is expressed and purified as a recombinant polypeptide, and a polypeptide or gene that interacts with that polypeptide is purified and screened based on binding. Alternatively, changes in binding activity can be monitored after adding a candidate inhibitor compound. In another method, the 5'-upstream transcription regulatory region of a gene that encodes a polypeptide of the present invention and that can regulate the

expression of another gene, is obtained. The gene is fused with a marker gene and then introduced into a cell, compounds and the like are added, and a factor which can regulate expression of that gene can be discovered.

5 A compound obtained by this screening can be used for developing pharmaceutical medicines for a disease in which a polypeptide of the present invention is involved. Similarly, if a regulatory factor obtained by screening turns out to be a polypeptide, compounds that can newly affect the expression or
10 activity of this polypeptide may be used as a medicine for diseases in which the polypeptide of the present invention is involved.

 If a polypeptide of the present invention has enzymatic activity, regardless of whether it is a secretory protein,
15 membrane protein, or a protein involved in signal transduction, glycoprotein, transcription, or disease, screening may be performed by adding a compound to the polypeptide of the present invention under suitable conditions, and monitoring that compound's change. This enzymatic activity may also be used as
20 an index to screen a compound that inhibits the polypeptide activity.

 In an example of this screening, a polypeptide of the present invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified
25 polypeptide, and the amount of compound and reaction product is examined. Alternatively, inhibitor candidate compounds are added, then a compound (substrate) that reacts with the purified polypeptide is added, and change in the amount of substrate and reaction product is examined.

30 A compound obtained by screening may be used as a medicine for diseases in which a polypeptide of the present invention is involved. Also such a compound can be applied in tests that examine, for example, whether a polypeptide of the invention functions normally *in vivo*.

35 Whether a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or

transcription-related protein of the present invention is a novel protein involved in disease or not is determined using different method to that described above. In this method, a specific antibody against a polypeptide of the present invention is obtained, and the relationship between the expression or activity of the polypeptide and a certain disease is examined. Alternatively, analysis can use the methods in "Molecular Diagnosis of Genetic Diseases" as a reference (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

Proteins involved in disease are very useful in developing drugs which regulate their expression and activity, and become targets of the above-mentioned screenings. They are also useful in the medicinal industry as diagnostic markers for their related disease, or as gene therapy targets.

A compound isolated as mentioned above can be administered to patients as is, or after being formulated into a pharmaceutical composition according to known methods. Specific examples of pharmaceutically acceptable carriers or vehicles include sterilized water, saline, plant oils, emulsifiers, suspending agents and the like, where they are mixed with the compound appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injection. Dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can properly choose an appropriate dosage. If a compound is encoded by a polynucleotide, the polynucleotide can be cloned into a gene therapy vector, and used for gene therapy. Those skilled in the art can properly choose the dosage of the polynucleotide and the method of its administration, and these may vary depending on the weight, age or symptoms of a patient.

The present invention further relates to databases comprising at least one sequence of a polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotides and/or amino acids

indicated in Table 1. The term "database" means a set of accumulated, machine-searchable and readable nucleotide sequence information. The databases of the present invention comprise at least one of the novel nucleotide sequences of the polynucleotides provided by the present invention. The databases of the present invention can consist only of the sequence data of the novel polynucleotides provided by the present invention, or can comprise other information on known nucleotide sequences of full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only information on nucleotide sequences, but also information on gene functions as revealed by the present invention. Additional information such as the names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

The database of the present invention is useful for gaining complete gene sequence information from the partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

Sequence information of the full-length cDNAs constituting the database of the present invention contains information on not only complete sequences, but also on gene expression frequency and gene homology to known genes and polypeptides. This extra information facilitates rapid functional analyses of partial gene fragments. Further, information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from another species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene
5 fragment corresponds to a known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there is no information corresponding to the partial sequence of interest in known databases, cDNA cloning should be carried out for the
10 full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using partial sequence information as an initial clue. If the full-length gene is not available, the amino acid sequence of the polypeptide encoded by that gene remains unidentified. Thus the database of the present
15 invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed using databases of known genes.

The present invention has provided 2,495 polynucleotides. In humans, where isolation of full-length cDNA has not
20 progressed, the provision of new full-length cDNAs has great significance. Secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are known to be involved in many diseases. The genes and proteins involved in
25 diseases are useful for developing diagnostic markers or medicines for regulation of their expression and activity, or as a gene therapy target.

In particular, cDNA encoding secretory proteins of the present invention are extremely important to the industry since
30 these proteins are expected to be useful as pharmaceutical agents, and many disease-related genes can be included with them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding these proteins can be used as
35 disease indexes, etc. These cDNAs are also very important to the industry, and are expected to be effective in treating

diseases and the like by regulating the activity or expression of the proteins they encode.

Human cDNAs involved in various diseases, morbid states, or functions were isolated in the present invention. The cDNAs of the present invention include, for example, genes that can be useful as diagnostic markers or therapeutic targets for the diseases or morbid states shown below. These diseases receive widespread attention, and require the development of new technology for treatment and diagnosis.

- 10 • osteoporosis
- neurologic diseases
- Alzheimer's disease
- Parkinson's disease
- dementia
- 15 • various cancers

In addition, human cDNAs involved in the functions shown below were isolated in the present invention. These genes can be used to elucidate the mechanisms of various functions, and in therapeutic methods which enhance or repress those functions. For example, genes participating in tissue generation and functional expression can be used in regenerative medicines.

- emotional reaction
- tissue generation and functional expression
- motor function controlled by the brain, signaling function controlled by the brain
- 25 • emotional reaction, fear response, and panic

Furthermore, information on the nucleotide sequence of the full-length cDNAs or their full-length amino acid sequences as provided by the present invention can be used to isolate human genes based on partial sequence information obtained by functional analysis of various genes, or from sequence information of genes from non-human organisms.

Any patents, patent applications, and publications cited herein are incorporated by reference.

35 The present invention is illustrated more specifically with reference to the following examples, but is not to be

construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

5 (1) Extraction and purchase of mRNA

Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989).
 10 Further, by the method described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) cultivated by the methods
 15 described in the catalogs.

The library names and origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

20 <Extraction of mRNA from human tissues>

NTONG: Normal tongue;

CTONG: Tongue cancer;

FCBBF: Fetal brain;

OCBBF: Fetal brain;

25 PLACE: Placenta;

SYNOV: Synovial membrane tissue (from rheumatioid arthritis);

CORDB: Cord blood.

<Extraction of mRNA from culture cells>

BNGH4: H4 cells (ATCC #HTB-148);

30 IMR32: IMR32 cells (ATCC #CCL-127);

SKNMC: SK-N-MC cells (ATCC #HTB-10);

3NB69: NB69 cells (RCB #RCB0480);

BGGI1: GI1 cells (RCB #RCB0763);

NB9N4: NB9 cells (RCB #RCB0477);

35 SKNSH: SK-N-SH cells (RCB #RCB0426);

AHMSC: Human mesenchymal cells (HMSC);

CHONS: Chondrocytes;
 ERLTF: TF-1 cells (Erythroleukemia);
 HELAC: HeLa cells;
 JCMLC: Myelogenous leukemia cells;
 5 MESTC: Mesenchyme stem cells;
 N1ESE: Mesenchymal stem cells;
 NCRRM: Embryonal carcinomas;
 NCRRP: Embryonal carcinomas treated with retinoic acid (RA) to induce the differentiation;
 10 T1ESE: Mesenchymal stem cells treated with trichostatin and 5-azacytidine to induce the differentiation;
 NT2RM: NT2 cells (STARATAGENE #204101);
 NT2RP: NT2 cells treated with RA for 5 weeks to induce the differentiation;
 15 NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks;
 NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron);
 20 NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for five weeks to induce the differentiation, and then treated with the growth inhibitor for two weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNA
 25 libraries whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01); the subtracted library (NT2RI-NT2RM) was provided by this procedure.

RCB indicates that the cell was provided by the Cell Bank,
 30 RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.

<Extraction of mRNA from primary culture cells>

ASTRO: Normal human astrocyte NHA5732, Takara Shuzo #CC2565;
 35 DFNES: Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;

- MESAN: Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;
- NHNPC: Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;
- 5 PEBLM: Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;
- HSYRA: Human synoviocyte HS-RA (from rheumatoid arthritis), Toyobo #T404K-05;
- PUAEN: Normal human pulmonary artery endothelial cells, Toyobo
- 10 #T302K-05;
- UMVEN: Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;
- HCASM: Normal human coronary artery smooth muscle cell HCASMC, Toyobo #T305K-05;
- 15 HCHON: Normal human chondrocyte HC, Toyobo #T402K-05;
- HHDPC: Normal human dermal papilla cell HDPC, Toyobo #THPCK-001;
- CD34C: CD34+ cells (AllCells, LLC #CB14435M);
- D3OST: CD34+ cells treated with the osteoclast differentiation factor (ODF) for three days to induce the differentiation;
- 20 D6OST: CD34+ cells treated with ODF for six days to induce the differentiation;
- D9OST: CD34+ cells treated with ODF for nine days to induce the differentiation;
- ACTVT: Activated T-cells;
- 25 LYMPB: Lymphoblasts (EB virus transferred B cells);
- NETRP: Neutrophils.

Total RNAs extracted from the following human tissues were then purchased and used as mRNA sources. Library names and the origins are indicated below in the order of "Library name:

30 Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

- 35 ADRGL: Adrenal gland, CLONTECH #64016-1;
- BRACE: Brain (cerebellum), CLONTECH #64035-1;

BRAWH: Whole brain, CLONTECH #64020-1;
FEBRA: Fetal brain, CLONTECH #64019-1;
FELIV: Fetal liver, CLONTECH #64018-1;
HEART: Heart, CLONTECH #64025-1;
5 HLUNG: Lung, CLONTECH #64023-1;
KIDNE: Kidney, CLONTECH #64030-1;
LIVER: Liver, CLONTECH #64022-1;
MAMGL: Mammary Gland, CLONTECH #64037-1;
PANCR: Pancreas, CLONTECH #64031-1;
10 PROST: Prostate, CLONTECH #64038-1;
SALGL: Salivary Gland, CLONTECH #64026-1;
SKMUS: Skeletal Muscle, CLONTECH #64033-1;
SMINT: Small Intestine, CLONTECH #64039-1;
SPLEN: Spleen, CLONTECH #64034-1;
15 STOMA: Stomach, CLONTECH #64090-1;
TBAES: Breast (Tumor), CLONTECH #64015-1;
TCERX: Cervix (Tumor), CLONTECH #64010-1;
TCOLN: Colon (Tumor), CLONTECH #64014-1;
TESTI: Testis, CLONTECH #64027-1;
20 THYMU: Thymus, CLONTECH #64028-1;
TLUNG: Lung (Tumor), CLONTECH #64013-1;
TOVAR: Ovary (Tumor), CLONTECH #64011-1;
TRACH: Trachea, CLONTECH #64091-1;
TUTER: Uterus (Tumor), CLONTECH #64008-1;
25 UTERU: Uterus, CLONTECH #64029-1;
ADIPS: Adipose, Invitrogen #D6005-01;
BLADE: Bladder, Invitrogen #D6020-01;
BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex,
Alzheimer), Invitrogen #D6830-01;
30 CERVX: Cervix, Invitrogen #D6047-01;
COLON: Colon, Invitrogen #D6050-0;
NESOP: Esophagus, Invitrogen #D6060-01;
PERIC: Pericardium, Invitrogen #D6105-01;
RECTM: Rectum, Invitrogen #D6110-01;
35 TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
TKIDN: Kidney (Tumor), Invitrogen #D6870-01;

TLIVE: Liver (Tumor), Invitrogen #D6880-01;
 TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
 BEAST: Adult breast, STARATAGENE #735044;
 FEHRT: Fetal heart, STARATAGENE #738012;
 5 FEKID: Fetal kidney, STARATAGENE #738014;
 FELNG: Fetal lung, STARATAGENE #738020;
 NOVAR: Adult ovary, STARATAGENE #735260;
 BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was
 constructed from mRNA prepared from tissues of cerebral cortex
 10 obtained from an Alzheimer patient [BRALZ: Cerebral cortex from
 an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen
 #D6830-01]; the cDNA libraries whose nucleotide sequences were
 shared by those of mRNAs from whole brain tissue [BRAWH: Whole
 brain, CLONTECH #64020-1] were subtracted using a Subtract Kit
 15 (Invitrogen #K4320-01).

Further, mRNAs extracted and purified as poly A(+) RNAs
 from the human tissues shown below were purchased. A cDNA
 library was prepared from an RNA mixture in which the poly A(+) RNA
 from each tissue was combined with poly A(-) RNA. The poly
 20 A(-) RNA was prepared by removing poly A(+) RNA from the total
 RNA of whole brain tissue (CLONTECH #64020-1) by using oligo dT
 cellulose. The library names and origins are indicated below in
 the order of "Library name: Origin".

<Purchase of mRNAs of human tissues as poly A(+) RNAs>

25 BRAMY: Brain (amygdala), CLONTECH #6574-1;
 BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
 BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
 BRHIP: Brain (hippocampus), CLONTECH #6578-1;
 BRSSN: Brain (substantia nigra), CLONTECH #6580-1;
 30 BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;
 BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA libraries

A cDNA library was prepared from each RNA using the
 35 improved method (WO 01/04286) of oligo capping [M. Maruyama and
 S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures,

BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (agcaucgagu cggccuuguu ggccuacugg/ SEQ ID NO: 4991) and oligo dT primer (gcggtgaag acggcctatg tggccttttt tttttttttt tt/ SEQ ID NO: 4992), as described in WO 01/04286. The single-stranded cDNA was then converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (agcatcgagt cggccttggtg/ SEQ ID NO: 4993) and 3' (gcggtgaag acggcctatg t/ SEQ ID NO: 4994) PCR primers, and then digested with *Sfi*I. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dra*III-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); and the cDNA library was thus prepared.

Shown below are the names of cDNA libraries used in the analysis of full-length cDNA sequences, and their origins. The Library Name is provided with the Type, Origin, and such of the library source, demarcated by a slash mark (/) within parentheses.

3NB69 (culture cells / NB69 cells (RCB #RCB0480))
 ACTVT (primary culture cells / Activated T-cells(Activated T-cell))
 ADIPS (Tissues / Adipose (Invitrogen #D6005-01))
 ADRGL (Tissues / Adrenal gland (CLONTECH #64016-1))
 25 ASTRO (primary culture cells / Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565))
 BLADE (Tissues / Bladder (Invitrogen #D6020-01))
 BNGH4 (culture cells / H4 cells (ATCC #HTB-148))
 BRACE (Tissues / Brain (cerebellum) (CLONTECH #64035-1))
 30 BRALZ (Tissues / Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer) (Invitrogen #D6830-01))
 BRAMY (Tissues / Brain (amygdala) (CLONTECH #6574-1))
 BRASW (Tissues / subtracted library (BRALZ-BRAWH). The cDNAs from tissues of cerebral cortex obtained from an Alzheimer
 35 patient whose nucleotide sequences were shared by those of mRNAs from whole brain tissue were subtracted.

BRAWH (Tissues / Whole brain (CLONTECH #64020-1))
 BRCAN (Tissues / Brain (caudate nucleus) (CLONTECH #6575-1))
 BRCOC (Tissues / Brain (corpus callosum) (CLONTECH #6577-1))
 BRHIP (Tissues / Brain (hippocampus) (CLONTECH #6578-1))
 5 BRSSN (Tissues / Brain (substantia nigra) (CLONTECH #6580-1))
 BRSTN (Tissues / Brain (subthalamic nucleus) (CLONTECH #6581-1))
 BRTHA (Tissues / Brain (thalamus) (CLONTECH #6582-1))
 CERVX (Tissues / Cervix (Invitrogen #D6047-01))
 COLON (Tissues / Colon (Invitrogen #D6050-0))
 10 CORDB (Tissues / Cord blood)
 CTONG (Tissues / Tongue Cancer)
 D3OST (primary culture cells / CD34+ cells (treated with ODF for
 three days to induce the differentiation))
 DFNES (primary culture cells / Normal human dermal fibroblasts
 15 (neonatal skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509))
 ERLTF (culture cells / TF-1 cells (Erythroleukemia))
 FCBBF (Tissues / Fetal brain)
 FEBRA (Tissues / Fetal brain (CLONTECH #64019-1))
 HCASM (primary culture cells / Normal human coronary artery
 20 smooth muscle cell HCASMC (Toyobo #T305K-05))
 HCHON (primary culture cells / Normal human chondrocyte HC
 (Toyobo #T402K-05))
 HEART (Tissues / Heart (CLONTECH #64025-1))
 HHDPC (primary culture cells / Normal human dermal papilla cell
 25 HDPC (Toyobo #THPCK-001))
 HLUNG (Tissues / Lung (CLONTECH #64023-1))
 HSYRA (primary culture cells / Human synoviocyte HS-RA (from
 rheumatoid arthritis) (Toyobo #T404K-05))
 IMR32 (culture cells / IMR32 cells (ATCC #CCL-127))
 30 KIDNE (Tissues / Kidney (CLONTECH #64030-1))
 LIVER (Tissues / Liver (CLONTECH #64022-1))
 LYMPB (primary culture cells / Lymphoblasts (EB virus
 transferred B cells))
 MESAN (primary culture cells / Normal human mesangial cell
 35 NHMC56046-2 (Takara Shuzo #CC2559))
 MESTC (culture cells / Mesenchyme stem cells)

NB9N4 (culture cells / NB9 cells (RCB #RCB0477))
 NCRRP (culture cells / Embryonal carcinomas treated with RA to induce the differentiation)
 NESOP (Tissues / Esophagus (Invitrogen #D6060-01))
 5 NHNPC (primary culture cells / Normal human neural progenitor cell NHNP5958 (Takara Shuzo #CC2599))
 NOVAR (Tissues / Adult ovary (STARATAGENE #735260))
 NT2NE (culture cells / NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the
 10 resultant neurons were concentrated and harvested (NT2 Neuron))
 NT2RI (culture cells / NT2 cells treated with RA for five weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks)
 NT2RP (culture cells / NT2 cells treated with RA for five weeks
 15 to induce the differentiation)
 NTONG (Tissues / Normal tongue)
 OCBBF (Tissues / Fetal brain)
 PEBLM (primary culture cells / Normal human peripheral blood mononuclear cell HPBMC5939 (Takara Shuzo #CC2702))
 20 PERIC (Tissues / Pericardium (Invitrogen #D6105-01))
 PLACE (Tissues / Placenta)
 PROST (Tissues / Prostate (CLONTECH #64038-1))
 PUAEN (primary culture cells / Normal human pulmonary artery endothelial cells (Toyobo #T302K-05))
 25 RECTM (Tissues / Rectum (Invitrogen #D6110-01))
 SKMUS (Tissues / Skeletal Muscle (CLONTECH #64033-1))
 SKNMC (culture cells / SK-N-MC cells (ATCC #HTB-10))
 SKNSH (culture cells / SK-N-SH cells (RCB #RCB0426))
 SMINT (Tissues / Small Intestine (CLONTECH #64039-1))
 30 SPLEN (Tissues / Spleen (CLONTECH #64034-1))
 STOMA (Tissues / Stomach (CLONTECH #64090-1))
 SYNOV (Tissues / Synovial membrane tissue (from rheumatoid arthritis))
 T1ESE (culture cells / Mesenchymal stem cell (treated with
 35 trichostatin and 5-azacytidine to induce the differentiation))
 TBAES (Tissues / Breast (Tumor) (CLONTECH #64015-1))

TCERX (Tissues / Cervix (Tumor) (CLONTECH #64010-1))
 TCOLN (Tissues / Colon (Tumor) (CLONTECH #64014-1))
 TESOP (Tissues / Esophageal (Tumor) (Invitrogen #D6860-01))
 TESTI (Tissues / Testis (CLONTECH #64027-1))
 5 THYMU (Tissues / Thymus (CLONTECH #64028-1))
 TKIDN (Tissues / Kidney (Tumor) (Invitrogen #D6870-01))
 TLIVE (Tissues / Liver (Tumor) (Invitrogen #D6880-01))
 TOVAR (Tissues / Ovary (Tumor) (CLONTECH #64011-1))
 TRACH (Tissues / Trachea (CLONTECH #64091-1))
 10 TSTOM (Tissues / Stomach (Tumor) (Invitrogen #D6920-01))
 TUTER (Tissues / Uterus (Tumor) (CLONTECH #64008-1))
 UTERU (Tissues / Uterus (CLONTECH #64029-1))

cDNA libraries with a high fullness ratio (the fullness ratio of 5'-end was 90% on average, calculated for each cDNA library using the protein coding region found in known mRNA species as an index) prepared by the improved oligo-capping method were constructed using a eukaryotic expression vector pME18SFL3. The vector contained SR α promoter and SV40 small t intron upstream of the cloning site, and SV40 polyA added signal sequence site downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, clones can be analyzed very easily using the clone gene product proteins, or those proteins' biological activities.

30 (3) Assessment of 5'-end completeness of clones derived from a cDNA library prepared by oligo-capping

With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction were conducted using a DNA sequencing reagent (BigDye Terminator

Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

5 The 5'-end completeness of about 1,110,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined using the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the
10 known human mRNA. Even if the 5'-end sequence was shorter, clones containing the translation initiation codon were judged to comprise the "full-length" sequence. Clones which did not comprise the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparison with known human mRNA. The fullness ratio of the 5'-ends was found to be 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in
15 human cDNA clones obtained by the oligo-capping method.
20

EXAMPLE 2

Sequencing analysis of cDNA ends and selection of full-length clones

25 With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready
30 Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

35 For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to

certain human mRNA sequences, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

EXAMPLE 3

Analysis of the full-length nucleotide sequences

The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

5

EXAMPLE 4

Functional prediction by homology search

GenBank, SwissProt, UniGene, RefSeq, and nr were searched using BLAST for the determined nucleotide sequences (SEQ ID NOs: 1-2188) and the ORF amino acid sequences deduced to encode the polypeptides (SEQ ID NOs: 2189-4376). SwissProt, RefSeq, and nr were searched using BLAST for the nucleotide sequences of SEQ ID NOs: 4377-4683, and the amino acid sequences of SEQ ID NOs: 4684-4990. Of the hit data which met the criteria described below, representative hit data were selected. This representative data is hit data with a higher homology and that enables relatively easy functional prediction for nucleotide sequences and deduced amino acid sequences. The results of the homology search are shown at the end of this specification.

- 20 · Hit data whose P value or E value is 10^{-4} or less
- For analysis using an amino acid database, hit data whose P value or E value is 10^{-4} or less, where the length of consensus sequence \times homology = 30 or higher,

Thus, only representative data are indicated and molecules exhibiting homology to each clone are not limited thereto. For some clones, hit data that do not meet the above-described criteria in BLAST search are not shown.

EXAMPLE 5

Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino

35

terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (Version 5.5) (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). In addition, the functional domain search can also be carried out on the PROSITE.

The search results obtained with the respective programs are shown below.

The 161 clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADIPS2000088, ADRGL2000172, ADRGL2009146, BNGH42003570,
 BRACE2030341, BRACE2031531, BRACE2039327, BRACE2041200,
 BRACE2043142, BRACE3004113, BRACE3004843, BRACE3010397,
 BRACE3011505, BRACE3026735, BRACE3040856, BRAMY2004771,
 BRAMY2005052, BRAMY2019300, BRAMY2019963, BRAMY3007206,
 BRAMY3007609, BRAMY3008505, BRAWH2002560, BRAWH3001475,
 BRAWH3003992, BRAWH3004666, BRAWH3006548, BRCAN2002948,
 BRCAN2010376, BRCAN2012481, BRHIP2005236, BRHIP2026288,
 BRHIP3008598, BRSSN2014424, BRSTN2007000, BRSTN2010363,
 BRSTN2016470, BRTHA2002608, BRTHA2005579, BRTHA2016496,
 BRTHA2018344, BRTHA3000633, BRTHA3017047, COLON2000568,
 COLON2002443, COLON2005126, CTONG1000302, CTONG1000488,
 CTONG1000508, CTONG2000042, CTONG2008233, CTONG3000707,
 CTONG3001560, CTONG3003179, CTONG3003483, CTONG3003737,
 CTONG3005648, CTONG3008258, CTONG3009385, D3OST2002182,
 D3OST2002648, FCBBF2001183, FCBBF2007510, FCBBF3009888,

FCBBF4000076, FEBRA2025427, HCASM2002502, HCHON2001577,
 HCHON2002676, HEART2001680, HSYRA2009102, IMR322002110,
 KIDNE2000846, KIDNE2006580, KIDNE2013095, LYMPB2000083,
 NOVAR2000136, NOVAR2001108, NT2RI2008724, NT2RI3005403,
 5 NT2RI3007065, NT2RP7000359, NT2RP7000466, NTONG2000413,
 OCBBF2006764, PLACE5000171, PLACE5000282, PLACE6012574,
 PROST2018090, PUAEN2002489, PUAEN2009795, RECTM2000433,
 SKMUS2000757, SKNMC2002402, SMINT2015787, SPLEN2009548,
 SPLEN2012624, SPLEN2012889, SPLEN2021701, SPLEN2030479,
 10 SPLEN2031125, SPLEN2034021, SPLEN2034781, SPLEN2037722,
 SPLEN2040222, STOMA2004294, SYNOV4002883, SYNOV4008336,
 TESOP2002273, TESOP2005485, TESOP2007636, TESTI2002618,
 TESTI2036684, TESTI2048898, TESTI4001561, TESTI4001665,
 TESTI4008401, TESTI4008797, TESTI4014392, TESTI4020102,
 15 TESTI4025797, TESTI4028429, TESTI4035065, TESTI4035649,
 TESTI4042711, TESTI4046487, THYMU2001053, THYMU2003632,
 THYMU2005321, THYMU2013386, THYMU2014353, THYMU2019210,
 THYMU2027497, THYMU2027695, THYMU2029676, THYMU2039780,
 THYMU2040412, THYMU3004835, THYMU3005696, THYMU3007845,
 20 TKIDN2002424, TKIDN2019116, TLIVE2002690, TRACH2007834,
 TRACH3002650, TRACH3004786, TRACH3006149, TRACH3035199,
 TRACH3035526, UTERU1000339, UTERU2025645, UTERU2026090,
 UTERU3000645, UTERU3000899, UTERU3001585, UTERU3002209,
 UTERU3002383, UTERU3003776, UTERU3009690, UTERU3009979,
 25 UTERU3015500

Deduced amino acid sequences of following 20 clones were also detected to have the signal sequences by PSORT.

BRACE2002589, BRACE2009318, BRACE2039823, BRAWH2006395,
 BRAWH2008993, BRCOC2019841, BRHIP2005271, BRTHA2011321,
 30 FEBRA2028256, HCASM2003099, PROST2000452, PROST2019487,
 SPLEN2016932, STOMA2003158, SYNOV2001660, SYNOV4003981,
 TESTI2015626, TESTI4000319, TKIDN2018926, UTERU2032279

The 523 clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid sequences. Of the search

result, the Clone Name and the Number of transmembrane domains are demarcated by a double slash mark (//).

ACTVT2000380//1, ADRGL2003329//2, ASTRO2014923//6,
 ASTRO3000301//1, BLADE1000176//1, BLADE2002073//1,
 5 BLADE2002947//2, BLADE2004462//2, BLADE2004670//1,
 BLADE2008539//1, BNGH42003570//1, BRACE1000186//1,
 BRACE2005457//8, BRACE2014306//11, BRACE2016981//1,
 BRACE2030341//1, BRACE2030884//3, BRACE2031527//1,
 BRACE2031899//2, BRACE2032385//3,
 10 BRACE2036005//1, BRACE2040138//2, BRACE2043142//4,
 BRACE2043665//1, BRACE3000697//4, BRACE3001391//3,
 BRACE3002298//1, BRACE3003004//1, BRACE3004113//1,
 BRACE3004843//1, BRACE3006462//3, BRACE3008384//6,
 BRACE3009574//1, BRACE3009708//6, BRACE3010397//2,
 15 BRACE3011505//2, BRACE3013740//3, BRACE3014005//8,
 BRACE3014068//3, BRACE3014807//3,
 BRACE3020286//3, BRACE3020594//2, BRACE3024662//1,
 BRACE3025531//1, BRACE3026008//2, BRACE3031838//1,
 BRACE3040856//3, BRALZ2016085//10, BRAMY2004771//2,
 20 BRAMY2005052//2, BRAMY2017528//1, BRAMY2019300//2,
 BRAMY2019963//1, BRAMY2028856//2, BRAMY2033003//2,
 BRAMY2033116//2, BRAMY2033594//1, BRAMY2036396//2,
 BRAMY2039872//2, BRAMY2040592//2,
 BRAMY2041542//1, BRAMY2045036//1, BRAMY2047420//1,
 25 BRAMY2047765//3, BRAMY3002312//1, BRAMY3004224//2,
 BRAMY3004919//5, BRAMY3008505//2, BRASW1000125//2,
 BRAWH2002560//1, BRAWH2002761//3, BRAWH2007658//2,
 BRAWH2014414//1, BRAWH2016439//1, BRAWH2016702//3,
 BRAWH3000078//2, BRAWH3000314//1, BRAWH3001891//6,
 30 BRAWH3002600//1, BRAWH3003555//2,
 BRAWH3003727//1, BRAWH3004453//1, BRAWH3004666//2,
 BRAWH3005132//1, BRAWH3005912//1, BRAWH3006548//2,
 BRAWH3007221//2, BRAWH3007506//2, BRAWH3007592//1,
 BRAWH3008634//1, BRCAN2012355//5, BRCAN2012481//1,
 35 BRCAN2013655//3, BRCAN2014143//5, BRCAN2028355//4,
 BRCOC2007034//2, BRCOC2019934//2, BRHIP2000691//1,

BRHIP2001805//1, BRHIP2002172//8,
 BRHIP2004814//1, BRHIP2004883//2, BRHIP2005752//2,
 BRHIP2009414//7, BRHIP2013699//1, BRHIP2026288//2,
 BRHIP3000526//1, BRHIP3007483//2, BRHIP3007586//1,
 5 BRHIP3008598//3, BRHIP3015751//1, BRHIP3024118//7,
 BRHIP3026097//1, BRSSN2003086//1, BRSSN2008549//1,
 BRSSN2011738//2, BRSSN2014424//9, BRSSN2018925//2,
 BRSTN2003835//1, BRSTN2007000//1,
 BRSTN2012380//1, BRSTN2015015//2, BRSTN2016678//3,
 10 BRSTN2017110//2, BRTHA2002281//2, BRTHA2002376//2,
 BRTHA2002493//1, BRTHA2002608//2, BRTHA2002808//1,
 BRTHA2003110//2, BRTHA2003461//3, BRTHA2006075//2,
 BRTHA2011194//1, BRTHA2012980//2, BRTHA2013460//2,
 BRTHA2015696//2, BRTHA2015878//2, BRTHA2016215//1,
 15 BRTHA2017985//1, BRTHA2018344//3,
 BRTHA2018624//1, BRTHA3000633//2, BRTHA3002427//12,
 BRTHA3003474//2, BRTHA3007148//3, BRTHA3008386//4,
 BRTHA3008778//1, BRTHA3009090//1, BRTHA3009291//2,
 BRTHA3016845//2, BRTHA3017047//2, BRTHA3017589//2,
 20 BRTHA3017848//8, BRTHA3018656//9, CERVX2002006//1,
 COLON2002443//1, COLON2005126//2, CTONG1000302//1,
 CTONG1000341//1, CTONG2004062//4,
 CTONG2008233//2, CTONG2009423//3, CTONG2009531//1,
 CTONG2013178//1, CTONG2019652//1, CTONG2019788//1,
 25 CTONG2020127//1, CTONG2020522//1, CTONG2020638//6,
 CTONG2022601//2, CTONG2023512//2, CTONG2026920//1,
 CTONG2027327//1, CTONG2028124//3, CTONG2028687//2,
 CTONG3001560//4, CTONG3002020//2, CTONG3002412//3,
 CTONG3003483//2, CTONG3003737//1,
 30 CTONG3008252//1, CTONG3008496//2, CTONG3008566//1,
 CTONG3008951//2, CTONG3009227//1, CTONG3009239//3,
 CTONG3009328//5, CTONG3009385//4, D3OST2002648//6,
 DFNES1000107//1, DFNES2010502//3, FCBBF2001183//2,
 FCBBF2007510//2, FCBBF3003435//1, FCBBF3004502//10,
 35 FCBBF3009888//1, FCBBF3012170//1, FCBBF3021576//1,
 FCBBF3023895//1, FEBRA2007544//1,

FEBRA2007708//13, FEBRA2008311//7, FEBRA2020668//2,
 FEBRA2025427//1, FEBRA2027082//1, HCASM2003212//1,
 HCASM2007047//9, HCHON2000212//1, HCHON2001084//12,
 HCHON2001548//1, HCHON2001712//9, HCHON2004007//3,
 5 HCHON2005921//4, HLUNG2000014//1, HLUNG2003872//5,
 HLUNG2010464//4, HLUNG2015617//2, HLUNG2017350//4,
 HSYRA2005496//2, HSYRA2006873//1,
 HSYRA2008714//6, HSYRA2009102//10, IMR322000127//2,
 IMR322002110//1, IMR322006222//1, KIDNE1000064//10,
 10 KIDNE2000832//10, KIDNE2000846//5, KIDNE2006580//1,
 KIDNE2010264//1, KIDNE2011635//12, KIDNE2012945//1,
 KIDNE2013095//3, LIVER2007415//1, LYMPB2000083//3,
 MESAN2001979//3, MESAN2012054//2, MESTC1000042//1,
 NHNPC2000606//1, NHNPC2001223//1,
 15 NT2RI2008724//1, NT2RI2009855//3, NT2RI3001263//1,
 NT2RI3003095//3, NT2RI3003382//1, NT2RI3003409//1,
 NT2RI3005403//2, NT2RI3006673//1, NT2RI3007065//3,
 NT2RI3007543//2, NT2RI3007978//2, NT2RP7000466//1,
 NT2RP7009030//1, NT2RP7014005//2, NTONG2000413//1,
 20 OCBBF2006151//5, OCBBF2006567//1, OCBBF2006764//1,
 OCBBF2007114//1, OCBBF2007428//1,
 OCBBF2009926//2, OCBBF2010140//13, OCBBF2017516//2,
 OCBBF2021788//1, OCBBF2024719//1, OCBBF2025458//2,
 OCBBF2030517//2, OCBBF2030574//3, OCBBF2031167//1,
 25 OCBBF2033869//2, OCBBF2038317//2, OCBBF3000483//1,
 OCBBF3003320//6, OCBBF3004314//1, PEBLM2000170//1,
 PEBLM2000338//2, PEBLM2002594//2, PEBLM2006113//1,
 PEBLM2007834//1, PERIC2001227//1,
 PERIC2003452//3, PERIC2004909//2, PERIC2006035//7,
 30 PERIC2007914//3, PLACE5000171//1, PLACE5000260//2,
 PLACE6012574//2, PLACE7000514//1, PLACE7001022//1,
 PROST1000184//2, PROST1000528//2, PROST1000559//1,
 PROST2018902//1, PROST2018922//1, PUAEN2002489//4,
 PUAEN2005588//1, PUAEN2006701//3, PUAEN2009174//1,
 35 PUAEN2009852//1, RECTM2001347//2,
 SMINT1000192//1, SMINT2002743//2, SMINT2009902//4,

SMINT2015787//2, SPLEN2001599//1, SPLEN2009548//2,
 SPLEN2012889//3, SPLEN2015158//1, SPLEN2015679//1,
 SPLEN2021701//2, SPLEN2023733//7, SPLEN2023791//1,
 SPLEN2025491//1, SPLEN2029522//1, SPLEN2029683//2,
 5 SPLEN2030335//1, SPLEN2030479//1, SPLEN2031125//2,
 SPLEN2031424//2, SPLEN2031547//6,
 SPLEN2031724//3, SPLEN2031780//2, SPLEN2032813//2,
 SPLEN2033098//1, SPLEN2036326//4, SPLEN2037722//2,
 SPLEN2038180//2, SPLEN2038345//1, SPLEN2040222//4,
 10 SPLEN2041304//1, SPLEN2042598//3, STOMA2008546//3,
 SYNOV2005817//2, SYNOV2012326//2, SYNOV2016124//1,
 SYNOV2021320//2, SYNOV4003322//3, SYNOV4004184//1,
 SYNOV4004741//3, SYNOV4004914//1,
 SYNOV4006256//2, SYNOV4007430//1, SYNOV4007553//2,
 15 SYNOV4007671//1, SYNOV4008336//2, SYNOV4008440//4,
 TCERX2000613//1, TESOP2000801//1, TESOP2001345//2,
 TESOP2001865//2, TESOP2002273//2, TESOP2002539//3,
 TESOP2005579//1, TESOP2006041//1, TESOP2007052//1,
 TESOP2007262//1, TESOP2007636//2, TESTI1000257//11,
 20 TESTI1000348//3, TESTI2002036//6,
 TESTI2002618//2, TESTI2002928//1, TESTI2003347//2,
 TESTI2005610//1, TESTI2006648//6, TESTI2013382//3,
 TESTI2024567//5, TESTI2034953//1, TESTI2034997//1,
 TESTI2035997//1, TESTI2042450//1, TESTI2047071//2,
 25 TESTI2048898//2, TESTI2051767//3, TESTI2052822//1,
 TESTI4000215//2, TESTI4000724//11, TESTI4001176//1,
 TESTI4001561//2, TESTI4001923//1,
 TESTI4002552//4, TESTI4002754//3, TESTI4005805//1,
 TESTI4005961//1, TESTI4006053//1, TESTI4006137//2,
 30 TESTI4007064//3, TESTI4007163//3, TESTI4007239//1,
 TESTI4007382//1, TESTI4008401//1, TESTI4009608//1,
 TESTI4013369//3, TESTI4013667//2, TESTI4013830//3,
 TESTI4016238//2, TESTI4017575//2, TESTI4017901//2,
 TESTI4018835//2, TESTI4019566//2,
 35 TESTI4020092//1, TESTI4020102//2, TESTI4021478//7,
 TESTI4023722//2, TESTI4024420//1, TESTI4024874//3,

TESTI4024890//2, TESTI4026456//1, TESTI4026785//1,
 TESTI4027821//1, TESTI4028062//1, TESTI4028429//1,
 TESTI4028823//4, TESTI4028880//11, TESTI4029836//7,
 TESTI4030159//3, TESTI4030505//2, TESTI4034172//3,
 5 TESTI4035649//2, TESTI4037244//1,
 TESTI4041053//2, TESTI4042711//2, TESTI4046487//1,
 THYMU2003632//4, THYMU2003760//1, THYMU2005003//2,
 THYMU2005303//1, THYMU2007658//2, THYMU2009425//3,
 THYMU2011548//6, THYMU2013386//2, THYMU2014353//2,
 10 THYMU2019210//2, THYMU2030068//3, THYMU2032035//2,
 THYMU2032437//1, THYMU2032655//1, THYMU2033308//1,
 THYMU2033816//4, THYMU2034314//1,
 THYMU2035064//2, THYMU2036085//6, THYMU2037226//3,
 THYMU2037233//1, THYMU2037348//2, THYMU2038772//1,
 15 THYMU2038797//1, THYMU2040412//1, THYMU2041015//12,
 THYMU3000028//1, THYMU3000036//2, THYMU3004835//1,
 THYMU3006168//8, THYMU3006811//2, THYMU3007368//1,
 TKIDN2002424//2, TKIDN2002632//1, TKIDN2006525//2,
 TKIDN2009092//1, TKIDN2009889//1,
 20 TKIDN2014771//2, TKIDN2019116//4, TLIVE2000023//5,
 TLIVE2001828//2, TLIVE2001927//2, TLIVE2002336//1,
 TLIVE2002690//2, TLIVE2003381//4, TLIVE2004110//1,
 TOVAR2001281//1, TRACH1000205//6, TRACH2001549//1,
 TRACH2001684//2, TRACH2006387//6, TRACH2007059//1,
 25 TRACH2008300//1, TRACH2020525//4, TRACH2021964//2,
 TRACH2022553//2, TRACH2025535//1,
 TRACH2025911//1, TRACH3000014//1, TRACH3002064//1,
 TRACH3002650//2, TRACH3004786//4, TRACH3005294//1,
 TRACH3006149//1, TRACH3007391//1, TRACH3008629//2,
 30 TRACH3035199//3, TRACH3036193//1, TSTOM2000442//2,
 TUTER2000916//1, UTERU2004688//1, UTERU2004929//1,
 UTERU2006137//1, UTERU2006568//1, UTERU2007444//1,
 UTERU2020718//2, UTERU2022020//1,
 UTERU2025025//1, UTERU2025891//2, UTERU2026090//1,
 35 UTERU2026203//3, UTERU2027591//1, UTERU2029953//3,
 UTERU2031851//2, UTERU2035323//3, UTERU2035469//1,

UTERU3000645//4, UTERU3000899//2, UTERU3001240//4,
 UTERU3001571//2, UTERU3001585//2, UTERU3002209//3,
 UTERU3002786//1, UTERU3003116//1, UTERU3003776//1,
 UTERU3006308//3, UTERU3008671//1,
 5 UTERU3009690//1, UTERU3011063//10, UTERU3016789//2

Deduced amino acid sequences of following 70 clones were also detected to have the transmembrane domains by SOSUI.

BLADE2006830//8, BRACE2002589//1, BRACE2011677//2,
 BRACE2029396//2, BRACE2039823//3, BRACE2039832//1,
 10 BRAMY2019111//5, BRAMY2045471//2, BRAWH2008993//1,
 BRHIP2003272//1, BRHIP2005724//1, BRHIP2008389//3,
 BRTHA2011321//2, BRTHA2017972//1, BRTHA2018011//2,
 BRTHA2018443//6, BRTHA3008826//1, CTONG2003348//1,
 CTONG2015633//2, CTONG2016942//1,
 15 CTONG2019822//9, CTONG2020974//1, FEBRA2000790//1,
 FEBRA2006519//1, FEBRA2008692//1, FEBRA2028516//2,
 HCASM2002754//4, HCASM2003099//3, HEART2009680//7,
 HLUNG2013350//1, HLUNG2015418//3, IMR322013396//2,
 LIVER2000247//4, NT2RI2009583//8, NT2RI2027157//6,
 20 OCBBF2030116//2, PLACE7000502//2, PROST2019487//2,
 SPLEN2016932//1, SPLEN2037319//2,
 SYNOV2001660//1, SYNOV2013637//4, SYNOV4003981//1,
 SYNOV4005889//1, TBAES2000932//1, TESOP2001796//2,
 TESOP2006865//1, TESTI2029252//9, TESTI2032643//3,
 25 TESTI2050780//6, TESTI4000137//3, TESTI4000155//1,
 TESTI4006473//1, TESTI4013894//4, TESTI4014801//1,
 TESTI4032090//2, TESTI4041086//10, THYMU2004284//1,
 THYMU2030462//1, THYMU2033401//4,
 THYMU2034279//1, THYMU2035710//1, THYMU2040925//3,
 30 TKIDN2008778//1, TKIDN2012771//4, TRACH3000420//7,
 UTERU2011220//1, UTERU2021820//2, UTERU2032279//2,
 UTERU3015069//2

The 664 clones whose deduced amino acid sequences were detected to have functional domains with Pfam are as follows.

35 The search result is indicated as "Clone Name//Functional Domain Name". When the clone has Multiple Hit Functional Domains, they

are listed and demarcated by a double slash mark (//). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

- 3NB692002685// R3H domain
- 5 3NB692002806// short chain dehydrogenase
3NB692008729// Hrl repeat motif
ADIPS2000088// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain
ASTRO1000009// Delta-aminolevulinic acid dehydratase// FERM
- 10 domain (Band 4.1 family)
ASTRO2003960// F-box domain.
ASTRO2014923// Ion transport protein
ASTRO3000301// Transmembrane 4 family// Adenovirus E3 region
protein CR2
- 15 BLADE2005036// Zinc carboxypeptidase
BLADE2007958// WD domain, G-beta repeat// WD domain, G-beta
repeat// WD domain, G-beta repeat
BLADE2008539// Carbohydrate phosphorylases
BNGH42003570// EB module// Furin-like cysteine rich region//
- 20 Thrombospondin type 1 domain
BNGH42007788// WD domain, G-beta repeat// WD domain, G-beta
repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
WD domain, G-beta repeat// WD domain, G-beta repeat
BRACE1000258// PH domain// PH domain
- 25 BRACE2005457// Sulfate transporter family// Xanthine/uracil
permeases family
BRACE2006319// TRAF-type zinc finger// Squash family of serine
protease inhibitors// TRAF-type zinc finger
BRACE2008594// Eukaryotic protein kinase domain
- 30 BRACE2010489// LysM domain
BRACE2014306// Vesicular monoamine transporter// Ribosomal
protein L23// Sugar (and other) transporter// LacY proton/sugar
symporter
BRACE2014475// Amidase
- 35 BRACE2015314// Bacterial mutT protein
BRACE2016981// Fanconi anaemia group C protein// Bacterial

flagellin N-terminus
 BRACE2018762// WH1 domain// RanBP1 domain.// Streptomyces
 extracellular neutral protein// Formyl transferase// K-box
 region// Tropomyosins
 5 BRACE2026836// Calponin homology (CH) domain
 BRACE2027258// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat
 BRACE2030341// Kinase associated domain 1
 BRACE2035381// Lysophospholipase catalytic domain
 10 BRACE2035441// Spectrin repeat// Spectrin repeat// Spectrin
 repeat
 BRACE2038329// TS-N domain// UBA domain
 BRACE2041009// TBC domain
 BRACE2042550// Thrombospondin type 1 domain// Trypsin Inhibitor
 15 like cysteine rich domain// von Willebrand factor type C
 domain// Thrombospondin type 1 domain
 BRACE2043142// Glucose-6-phosphate dehydrogenase
 BRACE2044286// CRAL/TRIO domain.// Spectrin repeat
 BRACE2045300// Cofilin/tropomyosin-type actin-binding proteins
 20 BRACE2046295// Immunoglobulin domain// EGF-like domain
 BRACE2047011// DNA polymerase family B
 BRACE3000071// Ank repeat// Ank repeat// Ank repeat
 BRACE3000973// Leucine Rich Repeat
 BRACE3001002// Lipoprotein
 25 BRACE3001391// Latrophilin/CL-1-like GPS domain// PLAT/LH2
 domain// Regulator of G protein signaling domain
 BRACE3003192// EGF-like domain// EGF-like domain// EGF-like
 domain// EGF-like domain// Metallothionein// Keratin, high
 sulfur B2 protein// EGF-like domain// EGF-like domain// EGF-like
 30 domain// EGF-like domain// TB domain// EGF-like domain// EGF-
 like domain// EGF-like domain// TB domain// EGF-like domain//
 EGF-like domain
 BRACE3004058// FAD/NAD-binding Cytochrome reductase//
 Oxidoreductase FAD/NAD-binding domain
 35 BRACE3004150// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP

domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

BRACE3004772// SAM domain (Sterile alpha motif)

BRACE3004880// GLTT repeat (12 copies)// GLTT repeat (12 copies)// GLTT repeat (12 copies)// Keratin, high sulfur B2 protein

BRACE3006872// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

BRACE3007625// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Cytochrome P450

BRACE3008137// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).

BRACE3008384// Rhomboid family

BRACE3008720// GTP1/OBG family// ADP-ribosylation factor family

BRACE3009090// Beige/BEACH domain

BRACE3009708// E1-E2 ATPase// Na⁺/K⁺ ATPase C-terminus

BRACE3010397// SCP-like extracellular protein

BRACE3011421// Phorbol esters/diacylglycerol binding dom// Diacylglycerol kinase catalytic domain (presumed)// Diacylglycerol kinase accessory domain (presumed)// Ank repeat// Ank repeat

BRACE3013576// Hemagglutinin// SPRY domain// Zinc finger, C3HC4 type (RING finger)

BRACE3014005// Putative integral membrane protein

BRACE3015262// Cytochrome P450

BRACE3015521// EF hand

BRACE3016884// Keratin, high sulfur B2 protein// Flagellar L-ring protein

BRACE3019084// SAM domain (Sterile alpha motif)

BRACE3024073// 4Fe-4S iron sulfur cluster binding protein// lactate/malate dehydrogenase// Viral (Superfamily 1) RNA helicase// Ras family

BRACE3025630// Subtilase family

BRACE3027326// LGN motif, putative GEF specific for G-alpha// Rap/ran-GAP

BRACE3027478// Permeases for cytosine/purines, uracil
 BRALZ2014484// PH domain
 BRALZ2016085// Presenilin// Sugar (and other) transporter//
 Monocarboxylate transporter

5 BRAMY2001473// Death domain// ZU5 domain
 BRAMY2004771// Leucine Rich Repeat// Leucine rich repeat C-
 terminal domain// Leucine rich repeat N-terminal domain
 BRAMY2005052// Immunoglobulin domain
 BRAMY2019300// Leucine Rich Repeat// Leucine rich repeat C-
 10 terminal domain// Leucine rich repeat N-terminal domain
 BRAMY2021498// Thrombospondin type 1 domain// DnaJ central
 domain (4 repeats)// Thrombospondin type 1 domain//
 Thrombospondin type 1 domain// Thrombospondin type 1 domain//
 Thrombospondin type 1 domain

15 BRAMY2030109// Phorbol esters/diacylglycerol binding domain (C1
 domain)// PHD-finger
 BRAMY2031317// PDZ domain (Also known as DHR or GLGF).
 BRAMY2036567// SH3 domain
 BRAMY2039872// Interferon alpha/beta domain

20 BRAMY2040592// Transient receptor
 BRAMY2042760// PH domain// PH domain
 BRAMY2046989// TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// TPR Domain// TPR Domain
 BRAMY2047746// Sodium and potassium ATPases// Ank repeat// Ank
 25 repeat// Ank repeat
 BRAMY2047751// Regulator of G protein signaling domain// Raf-
 like Ras-binding domain// Raf-like Ras-binding domain
 BRAMY3001794// Geminivirus coat protein// PH domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 30 Leucine Rich Repeat// Leucine Rich Repeat
 BRAMY3002803// P21-Rho-binding domain// Eukaryotic protein
 kinase domain// Eukaryotic protein kinase domain
 BRAMY3004224// Leucine rich repeat N-terminal domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 35 Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat
 C-terminal domain

- BRAMY3004919// Copper/zinc superoxide dismutase (SODC)//
 Adenylate and Guanylate cyclase catalytic domain// Adenylate and
 Guanylate cyclase catalytic domain
 BRAMY3005091// Phosphatidylinositol 3- and 4-kinases
- 5 BRAMY3005932// Ank repeat
 BRAMY3008466// WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 WD domain, G-beta repeat// WD domain, G-beta repeat
 BRAMY4000095// Eukaryotic protein kinase domain
- 10 BRAMY4000277// Immunoglobulin domain// Immunoglobulin domain
 BRAWH1000127// Plexin repeat// Thrombospondin type 1 domain
 BRAWH2001395// Myelin basic protein
 BRAWH2001940// NOL1/NOP2/sun family
 BRAWH2007658// Immunoglobulin domain
- 15 BRAWH2010000// Xylose isomerase
 BRAWH2014414// Cadherin domain// Cadherin domain// Cadherin
 domain// Fructose-bisphosphate aldolase class-// Cadherin
 domain// Cadherin domain// Cadherin cytoplasmic region
 BRAWH2014662// K⁺ channel tetramerisation domain// ATP synthase
- 20 Alpha chain, C terminal
 BRAWH2014954// PDZ domain (Also known as DHR or GLGF).// PDZ
 domain (Also known as DHR or GLGF).
 BRAWH2016702// AMP-binding enzyme
 BRAWH3000078// Adaptin N terminal region// Activin types I and
- 25 II receptor domain
 BRAWH3000314// Fibronectin type III domain
 BRAWH3000491// Ribosomal protein S12e
 BRAWH3001326// Protein phosphatase 2C
 BRAWH3001891// YCF9
- 30 BRAWH3002574// Calpain large subunit, domain III// EF hand
 BRAWH3002600// Cadherin domain// Cadherin domain// Cadherin
 domain
 BRAWH3002821// C2 domain// C2 domain
 BRAWH3003727// ribonuclease.
- 35 BRAWH3005912// bZIP transcription factor// bZIP transcription
 factor// Troponin// TBC domain

BRAWH3008341// Pentaxin family
 BRCAN2002562// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 BRCAN2002856// Phosphotyrosine interaction domain (PTB/PID).
 5 BRCAN2002948// Adaptin N terminal region
 BRCAN2006063// von Willebrand factor type A domain
 BRCAN2009203// SAM domain (Sterile alpha motif)
 BRCAN2009432// ADP-ribosylation factor family// Ras family
 BRCAN2015464// Gag P30 core shell protein
 10 BRCAN2016619// SH3 domain
 BRCAN2017717// Squash family of serine protease inhibitors
 BRCAN2021028// Aminopeptidase I zinc metalloprotease (M18)
 BRCAN2024451// Raf-like Ras-binding domain// Leptin// Raf-like Ras-binding domain// LGN motif, putative GEF specific for G-
 15 alpha GTPase
 BRCAN2028355// Eukaryotic protein kinase domain
 BRCOC2001505// Myelin basic protein
 BRCOC2003213// ATP synthase, Delta/Epsilon chain// tRNA synthetase class II core domain (G, H, P, S and T)
 20 BRCOC2016525// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 BRHIP2000819// WD domain, G-beta repeat
 BRHIP2000920// Ribosomal protein S9/S16
 BRHIP2003786// Ank repeat// Ank repeat// Ank repeat// BTB/POZ
 25 domain
 BRHIP2004359// Metallo-beta-lactamase superfamily
 BRHIP2004814// Phosphate transporter family
 BRHIP2005236// Galactose binding lectin domain// Latrophilin
 Cytoplasmic C-terminal region
 30 BRHIP2005932// PH domain
 BRHIP2007616// Sema domain
 BRHIP2009414// Uncharacterized protein family
 BRHIP2021615// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 35 domain)
 BRHIP2026288// Prolyl oligopeptidase family// alpha/beta

hydrolase fold

BRHIP3000339// Myelin basic protein

BRHIP3008183// Adaptin N terminal region// tRNA (Guanine-1)-methyltransferase

5 BRHIP3008313// Ank repeat

BRHIP3008405// PH domain

BRHIP3024118// Sodium:galactoside symporter family//
Monocarboxylate transporter

BRHIP3025161// Phosphotriesterase family// RhoGEF domain// PH

10 domain// Thaumatin family// GATA zinc finger// FYVE zinc
finger// PH domain

BRHIP3027137// Aldehyde dehydrogenase family

BRSSN2000684// Protein-tyrosine phosphatase// Dual specificity phosphatase, catalytic domain

15 BRSSN2004719// Src homology domain 2

BRSTN2000872// Thioredoxin// Thioredoxin

BRSTN2001067// Rifin/stevor family

BRSTN2004863// Chitin synthase// Glycosyl transferases//
Similarity to lectin domain of ricin beta-chain, 3 copies.

20 BRSTN2004987// tRNA synthetases class I (W and Y)

BRSTN2008418// RhoGAP domain

BRSTN2013741// Ras family

BRTHA2000855// Extracellular link domain

BRTHA2004978// Collagen triple helix repeat (20 copies)

25 BRTHA2005579// von Willebrand factor type C domain// von

Willebrand factor type C domain// von Willebrand factor type C
domain// von Willebrand factor type C domain// von Willebrand
factor type C domain// von Willebrand factor type C domain// v
Willebrand factor type C domain// von Willebrand factor type C

30 domain// von Willebrand factor type C domain// von Willebrand
factor type C domain// von Willebrand factor type C domain// von
Willebrand factor type C domain

BRTHA2007122// Ank repeat// Ank repeat// Ank repeat// Ank repeat// SAM domain (Sterile alpha motif)

35 BRTHA2008527// Leucine Rich Repeat// Leucine Rich Repeat//

Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

- BRTHA2009311// Vertebrate galactoside-binding lectins
 BRTHA2010884// Thrombospondin type 1 domain// CUB domain
 BRTHA2012980// Cytochrome P450
 BRTHA2013262// Keratin, high sulfur B2 protein
 5 BRTHA2014792// SET domain
 BRTHA2015406// UBA domain
 BRTHA2015878// Gram-negative pili assembly chaperone
 BRTHA2016496// Peptidase C13 family
 BRTHA2018591// GTPase of unknown function
 10 BRTHA2018624// Galactose binding lectin domain// Activin types I
 and II receptor domain// Galactose binding lectin domain
 BRTHA2018707// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 BRTHA2019048// Domain of unknown function DUF71
 15 BRTHA3002401// Ornithine decarboxylase antizyme
 BRTHA3002427// Sulfate transporter family//
 Sodium:neurotransmitter symporter family
 BRTHA3003074// Fanconi anaemia group C protein
 BRTHA3003449// Myosin head (motor domain)
 20 BRTHA3005046// Collagen triple helix repeat (20 copies)
 BRTHA3008310// Homeobox domain
 BRTHA3008778// AMP-binding enzyme
 BRTHA3009037// C2 domain// PDZ domain (Also known as DHR or
 GLGF).// Regulator of G protein signaling domain// Regulator of
 25 G protein signaling domain
 BRTHA3009090// Cyclic nucleotide-binding domain// Cyclic
 nucleotide-binding domain// Cyclic nucleotide-binding domain//
 Glutathione S-transferases.// Uncharacterized protein family
 UPF0028
 30 BRTHA3013884// Domain associated with PX domains// PX domain//
 60s Acidic ribosomal protein
 BRTHA3015815// AIR synthase related protein
 BRTHA3016917// tRNA synthetases class I (C)// tRNA synthetases
 class I (I, L, M and V)
 35 BRTHA3017589// Immunoglobulin domain// Immunoglobulin domain//
 Hantavirus glycoprotein G2

- BRTHA3017848// Glucose-6-phosphate dehydrogenase// Sugar (and other) transporter
- BRTHA3018656// Divalent cation transporter// Divalent cation transporter
- 5 COLON2000568// Immunoglobulin domain// Cellulose binding domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- COLON2001721// C2 domain
- COLON2002520// Myosin head (motor domain)// IQ calmodulin-binding motif
- 10 COLON2004478// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- CORDB1000140// TRAF-type zinc finger
- 15 CORDB2000541// F-actin capping protein, beta subunit
- CTONG1000341// EGF-like domain// EGF-like domain// Metallothionein// EGF-like domain// EB module// EGF-like domain// EGF-like domain// EGF-like domain
- CTONG1000467// Zinc finger, C3HC4 type (RING finger)
- 20 CTONG2000042// Bacterial regulatory proteins, gntR family// Alpha-2-macroglobulin family N-terminal region// Alpha-2-macroglobulin family
- CTONG2001877// MutT-like domain
- CTONG2004062// E1-E2 ATPase
- 25 CTONG2006798// Eukaryotic protein kinase domain// Eukaryotic protein kinase domain
- CTONG2008233// DnaJ domain
- CTONG2009423// 7 transmembrane receptor (rhodopsin family)
- CTONG2013178// SEA domain// Trypsin
- 30 CTONG2017500// F-box domain.
- CTONG2020026// Herpesvirus VP23 like capsid protein
- CTONG2024206// Neuregulin family// von Willebrand factor type A domain// EGF-like domain// Response regulator receiver domain// von Willebrand factor type A domain// von Willebrand factor type A domain
- 35 A domain
- CTONG2024749// Alpha-2-macroglobulin family

- CTONG2025496// Alpha-2-macroglobulin family N-terminal region//
Alpha-2-macroglobulin family
- CTONG2028124// AMP-binding enzyme
- CTONG2028687// TPR Domain// TPR Domain
- 5 CTONG3000084// DNA mismatch repair protein// RhoGEF domain// PH
domain// SH3 domain
- CTONG3000657// SH3 domain
- CTONG3000686// TPR Domain// TPR Domain// TPR Domain// TPR Domain
- CTONG3001123// BRCA1 C Terminus (BRCT) domain// BRCA1 C Terminus
- 10 (BRCT) domain// BRCA1 C Terminus (BRCT) domain// BRCA1 C
Terminus (BRCT) domain// BRCA1 C Terminus (BRCT) domain
- CTONG3001370// Alpha-2-macroglobulin family N-terminal region//
Alpha-2-macroglobulin family
- CTONG3002127// C2 domain// C2 domain
- 15 CTONG3002674// Calponin homology (CH) domain
- CTONG3003737// Leucine rich repeat N-terminal domain// Leucine
Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
- 20 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
Repeat// Leucine Rich Repeat// Leucine rich repeat C-terminal
domain// Fusion glycoprotein F0.
- CTONG3003972// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
25 domain)
- CTONG3004072// Beta type Zein// Keratin, high sulfur B2 protein
- CTONG3005325// TS-N domain// UBA domain// Transposase
- CTONG3005648// Putative undecaprenyl diphosphate synthase
- CTONG3006067// DnaJ central domain (4 repeats)
- 30 CTONG3006186// PDZ domain (Also known as DHR or GLGF)//
Apolipoprotein A1/A4/E family// WW domain
- CTONG3008831// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
domain)
- CTONG3009028// Helicases conserved C-terminal domain
- 35 CTONG3009385// TPR Domain// TPR Domain// TPR Domain// TPR
Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR

Domain// TPR Domain
 D3OST2002182// Glycosyl transferase family 8
 D3OST2002648// 7 transmembrane receptor (rhodopsin family)// 7
 transmembrane receptor (rhodopsin family)
 5 D3OST3000169// SH3 domain// SAM domain (Sterile alpha motif)
 DFNES2000146// Plexin repeat// Thrombospondin type 1 domain
 DFNES2001108// PH domain
 DFNES2005266// Thrombospondin type 1 domain
 DFNES2011499// WD domain, G-beta repeat
 10 FCBBF3004502// Terpene synthase family// YCF9
 FCBBF3007540// RhoGEF domain// PH domain
 FCBBF3009888// Keratin, high sulfur B2 protein// u-PAR/Ly-6
 domain
 FCBBF3012170// Thrombospondin type 1 domain
 15 FCBBF3012288// Fibronectin type III domain
 FCBBF3013307// DEAD/DEAH box helicase// Helicases conserved C-
 terminal domain
 FEBRA2000253// Flagellar L-ring protein
 FEBRA2007708// Fusion glycoprotein F0.// Xanthine/uracil
 20 permeases family// Sulfate transporter family
 FEBRA2007801// IBR domain
 FEBRA2008311// 7 transmembrane receptor (rhodopsin family)// 7
 transmembrane receptor (rhodopsin family)
 FEBRA2008468// alpha/beta hydrolase fold
 25 FEBRA2021571// von Willebrand factor type D domain
 FEBRA2024150// DENN (AEX-3) domain
 FEBRA2026984// tRNA synthetases class I (W and Y)// Putative
 tRNA binding domain
 HCASM2001301// Eukaryotic protein kinase domain
 30 HCASM2002918// ATP synthase Alpha chain, C terminal
 HCHON2000028// RhoGAP domain
 HCHON2001084// FecCD transport family// Sugar (and other)
 transporter
 HCHON2001217// Cullin family
 35 HCHON2001577// Collagen triple helix repeat (20 copies)// Heavy-
 metal-associated domain

HCHON2001712// Sodium:dicarboxylate symporter family
 HCHON2002676// Glycosyl hydrolases family 39
 HCHON2004007// E1-E2 ATPase
 HCHON2004531// Ubiquitin family// UBA domain// Integrins, beta
 5 chain// UBA domain
 HCHON2004776// Protein of unknown function DUF93
 HCHON2005921// PMP-22/EMP/MP20/Claudin family
 HCHON2006250// WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
 10 HEART1000139// Troponin
 HEART2001680// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 HEART2001756// Bacterial transcriptional regulator
 15 HEART2006131// Thiamine pyrophosphate enzymes
 HEART2006909// CBS domain// CBS domain
 HEART2010495// Tau and MAP proteins, tubulin-binding
 HHDPC1000118// Adenylate kinase// Shikimate kinase//
 Deoxynucleoside kinase// Pyridoxal-phosphate dependent enzyme
 20 HLUNG1000017// Reprolysin family propeptide
 HLUNG2000014// Lectin C-type domain
 HLUNG2001996// SH3 domain
 HLUNG2002465// PH domain// RhoGEF domain// SH3 domain
 HLUNG2002958// EF hand
 25 HLUNG2011298// Oxidoreductase FAD/NAD-binding domain
 HLUNG2013851// Pumilio-family RNA binding domains (aka PUM-HD,
 Pumilio homology domain)// Pumilio-family RNA binding domains
 (aka PUM-HD, Pumilio homology domain)
 HLUNG2014262// von Willebrand factor type A domain// von
 30 Willebrand factor type A domain
 HLUNG2017350// Connexin
 HSYRA2005456// Fibronectin type III domain
 HSYRA2005496// emp24/gp25L/p24 family
 HSYRA2009075// Fibronectin type III domain
 35 HSYRA2009102// Integral membrane protein DUF6
 IMR322000127// Zinc finger, C2H2 type

IMR322000917// Zinc finger, C2H2 type
 IMR322006495// Tropomyosins
 KIDNE1000064// Integral membrane protein DUF7// Sugar (and
 other) transporter// Transmembrane 4 family// Zn-finger in Ran
 5 binding protein and others.
 KIDNE2000832// Amino acid permease// Transmembrane amino acid
 transporter protein// Sodium/hydrogen exchanger family
 KIDNE2000846// Sodium:neurotransmitter symporter family
 KIDNE2001361// Domain of unknown function DUF19
 10 KIDNE2001847// RhoGAP domain// SH3 domain
 KIDNE2006580// Cytochrome P450
 KIDNE2011635// Sodium:solute symporter family
 KIDNE2012945// CUB domain// Pentaxin family
 LYMPB2000083// Class I Histocompatibility antigen, domains alpha
 15 1 and 2// Class I Histocompatibility antigen, domains alpha 1
 and 2// Immunoglobulin domain
 MESAN2006563// PH domain
 MESAN2012054// PQQ enzyme repeat// PQQ enzyme repeat
 NESOP2001433// Immunoglobulin domain// Immunoglobulin domain//
 20 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 NESOP2001656// Polyomavirus coat protein
 NHNPC2001816// Regulator of G protein signaling domain
 NOVAR2000136// Thioredoxin// CTF/NF-I family// Calsequestrin
 25 NOVAR2001108// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 NT2NE2003252// Eukaryotic protein kinase domain
 NT2NE2006531// KRAB box// PHD-finger// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type
 30 NT2NE2006909// Influenza Matrix protein (M1)// metalloproteinase
 family M24
 NT2RI2004618// Cytosolic long-chain acyl-CoA thioesterase
 NT2RI2005166// F-box domain// WD domain, G-beta repeat
 NT2RI2008724// GGL domain
 35 NT2RI2025909// Mitochondrial carrier proteins// Mitochondrial
 carrier proteins// Mitochondrial carrier proteins

- NT2RI2025957// PDZ domain (Also known as DHR or GLGF).
- NT2RI3000622// TBC domain
- NT2RI3002842// Hsp20/alpha crystallin family
- NT2RI3003382// Rotavirus RNA-binding Protein 53 (NS53)
- 5 NT2RI3004510// Pyridine nucleotide-disulphide oxidoreductase//
FAD binding domain// Flavin containing amine oxidase// Phytoene
dehydrogenase related enzyme
- NT2RI3006171// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain
- 10 NT2RI3006340// Immunoglobulin domain// Immunoglobulin domain//
Fibronectin type III domain// Fibronectin type III domain//
Fibronectin type III domain// Fibronectin type III domain//
Fibronectin type III domain// Immunoglobulin domain// Ribosomal
protein S14p/S29e // Immunoglobulin domain// Immunoglobulin
- 15 domain
- NT2RI3006376// DENN (AEX-3) domain// PLAT/LH2 domain
- NT2RI3006673// Fibronectin type III domain// Fibronectin type
III domain// Fibronectin type III domain// Protein-tyrosine
phosphatase// Dual specificity phosphatase, catalytic domain//
- 20 Protein-tyrosine phosphatase
- NT2RI3007158// FYVE zinc finger
- NT2RI3007291// Collagen triple helix repeat (20 copies)
- NT2RI3007543// DnaJ domain
- NT2RI3007978// Glutamine amidotransferase class-I
- 25 NT2RI3008652// FERM domain (Band 4.1 family)// Uncharacterised
protein family UPF0058// Biopterin-dependent aromatic amino acid
hydroxylase
- NT2RP7000359// FERM domain (Band 4.1 family)// Insulin-like
growth factor binding proteins// PDZ domain (Also known as DHR
- 30 or GLGF).
- NT2RP7000466// CUB domain// CXXC zinc finger// EGF-like domain//
Granulins// Keratin, high sulfur B2 protein// Trypsin Inhibitor
like cysteine rich domain
- NT2RP7004027// CUB domain// Sushi domain (SCR repeat)
- 35 NT2RP7004123// Hepatitis delta virus delta antigen
- NT2RP7005118// GTPase-activator protein for Ras-like GTPase// IQ

[illegible]

repeat// Ank repeat
 OCBBF2008770// TBC domain
 OCBBF2010140// Alphavirus E1 glycoprotein
 OCBBF2010416// Major intrinsic protein
 5 OCBBF2019823// lactate/malate dehydrogenase
 OCBBF2020838// Fork head domain
 OCBBF2021323// Regulatory subunit of type II PKA R-subunit
 OCBBF2022351// WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 10 WD domain, G-beta repeat// WD domain, G-beta repeat
 OCBBF2025527// NAD-dependent glycerol-3-phosphate dehydrogenase
 OCBBF2031167// Reprolysin family propeptide// Pancreatic hormone
 peptides// Reprolysin (M12B) family zinc metalloprotease//
 Disintegrin// Beta defensin// Radical activating enzymes// EB
 15 module// EGF-like domain// Delta serrate ligand
 OCBBF2033869// CUB domain
 OCBBF2035110// PLAT/LH2 domain
 OCBBF2036743// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 20 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 25 C2H2 type// Zinc finger, C2H2 type
 OCBBF2037340// Alpha crystallin A chain, N terminal// Archaeal
 ATPase// Dual specificity phosphatase, catalytic domain
 OCBBF2037547// PH domain// Raf-like Ras-binding domain//
 Transaldolase// PDZ domain (Also known as DHR or GLGF).// RhoGEF
 30 domain// PH domain
 OCBBF2037598// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Fibronectin type III domain//
 Fibronectin type III domain
 OCBBF2037638// Pyridine nucleotide-disulphide oxidoreductase//
 35 Pyridine nucleotide-disulphide oxidoreductase
 OCBBF2038317// Syndecan domain// BNR repeat// BNR repeat// BNR

repeat// BNR repeat// BNR repeat// PKD domain
 OCBBF3009279// KH domain// Zinc finger, C3HC4 type (RING finger)
 PEBLM2002594// ABC transporter// Aldehyde oxidase and xanthine
 dehydrogenase, C terminus
 5 PEBLM2004666// WD domain, G-beta repeat// Gram-negative pili
 assembly chaperone// WD domain, G-beta repeat// WD domain, G-
 beta repeat// WD domain, G-beta repeat// WD domain, G-beta
 repeat// WD domain, G-beta repeat
 PERIC1000147// Syndecan domain
 10 PERIC2001228// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 PERIC2003720// Ezrin/radixin/moesin family
 PERIC2009086// 7 transmembrane receptor (rhodopsin family)//
 15 Peroxidase
 PLACE5000171// Chitin binding Peritrophin-A domain// HYR
 domain// Plant PEC family metallothionein// Sushi domain (SCR
 repeat)// von Willebrand factor type A domain
 PLACE5000282// Collagen triple helix repeat (20 copies)// Heavy-
 20 metal-associated domain
 PLACE6012574// ENV polyprotein (coat polyprotein)
 PLACE6019385// REV protein (anti-repression trans-activator
 protein)
 PLACE6020031// Ank repeat// Ank repeat
 25 PLACE7000514// Filamin/ABP280 repeat.
 PLACE7002641// LPP20 lipoprotein precursor// HRDC domain//
 Dihydrodipicolinate synthetase family
 PLACE7006051// ENV polyprotein (coat polyprotein)
 PLACE7008431// Phosphatidylinositol-4-phosphate 5-Kinase
 30 PROST1000184// 7 transmembrane receptor (Secretin family)
 PROST2008993// BRCA1 C Terminus (BRCT) domain
 PROST2016462// WW domain// PH domain// RhoGAP domain
 PROST2017367// Transglutaminase family
 PROST2018090// Sushi domain (SCR repeat)// Sushi domain (SCR
 35 repeat)// Chitin binding Peritrophin-A domain// HYR domain//
 Sushi domain (SCR repeat)

- PROST2018511// Ras association (RalGDS/AF-6) domain// PH domain// Src homology domain 2
- PUAEN2002616// Src homology domain 2
- PUAEN2005930// Extracellular link domain// PH domain
- 5 PUAEN2006328// TBC domain
- PUAEN2007044// TruB family pseudouridylate synthase (N terminal domain)
- PUAEN2009174// L1 (late) protein// Alpha-2-macroglobulin family
- PUAEN2009795// Ribosomal protein S3, C-terminal domain// EGF-like domain// Clq domain
- 10 PUAEN2009852// Eukaryotic protein kinase domain
- RECTM2000433// Jacalin-like lectin domain
- SKMUS2006394// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
- 15 SMINT1000192// Small hydrophilic plant seed proteins
- SMINT2002743// ENV polyprotein (coat polyprotein)
- SMINT2010076// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- 20 SMINT2011888// Immunoglobulin domain// Cellulose binding domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- SMINT2015787// Serum amyloid A protein// Immunoglobulin domain
- SPLEN2001599// Immunoglobulin domain
- 25 SPLEN2002147// Phosphatidylinositol transfer protein
- SPLEN2002467// DB module// F-box domain// Leucine Rich Repeat
- SPLEN2006122// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- 30 SPLEN2010912// DEAD/DEAH box helicase// Helicases conserved C-terminal domain
- SPLEN2012624// Ank repeat// Ank repeat// Ank repeat// Sodium:neurotransmitter symporter family
- SPLEN2015267// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- 35 SPLEN2015679// ATP synthase delta (OSCP) subunit

- SPLEN2021701// Class I Histocompatibility antigen, domains alpha 1 and 2// Class I Histocompatibility antigen, domains alpha 1 and 2// Immunoglobulin domain
 SPLEN2030335// AMP-binding enzyme
- 5 SPLEN2031547// Integral membrane protein// Integral membrane protein
 SPLEN2031780// Domain of unknown function DUF139// Domain of unknown function DUF139
 SPLEN2033098// TNFR/NGFR cysteine-rich region
- 10 SPLEN2034081// Insulin-like growth factor binding proteins
 SPLEN2036326// GPR1/FUN34/yaaH family// PMP-22/EMP/MP20/Claudin family
 SPLEN2036821// Mitochondrial carrier proteins
 SPLEN2037722// Immunoglobulin domain// Immunoglobulin domain
- 15 STOMA2004294// Immunoglobulin domain
 SYNOV2005448// Apidaecin
 SYNOV2005817// Domain of unknown function DUF19// Tissue factor
 SYNOV2006430// Nitrogen regulatory protein P-II
 SYNOV2014400// EGF-like domain// Granulins// Granulins// EGF-like domain
- 20 SYNOV2021320// Src homology domain 2
 SYNOV3000231// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
 SYNOV3000302// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
- 25 SYNOV4002392// lactate/malate dehydrogenase
 SYNOV4002883// Adenosylmethionine decarboxylase
 SYNOV4007521// Immunoglobulin domain// Immunoglobulin domain
 SYNOV4007553// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat
- 30 C-terminal domain// TIR domain
- 35 SYNOV4007671// Syntaxin// Fusion glycoprotein F0.
 SYNOV4008440// Adaptin N terminal region

- TBAES2001171// NOL1/NOP2/sun family
TBAES2001229// Ribosomal protein L23
TBAES2003550// Glucose-6-phosphate dehydrogenase
TBAES2004055// Ribosomal protein S11
- 5 TESOP2000801// Eukaryotic protein kinase domain
TESOP2001166// Src homology domain 2
TESOP2001953// Leucine Rich Repeat// Leucine Rich Repeat//
Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
Repeat// Leucine Rich Repeat// Leucine Rich Repeat
- 10 TESOP2004114// Lysyl hydrolase// Lysyl hydrolase
TESOP2005485// Immunoglobulin domain// Immunoglobulin domain
TESOP2009121// DNA polymerase (viral) C-terminal domain
TESTI1000257// GntP family permease// Sugar (and other)
transporter
- 15 TESTI1000390// Bromodomain// Atrial natriuretic peptide
TESTI1000545// TPR Domain// TPR Domain// TPR Domain// LPP20
lipoprotein precursor// HRDC domain// Adaptin N terminal
region// Dihydrodipicolinate synthetase family
TESTI2000443// Leucine Rich Repeat// Leucine Rich Repeat//
- 20 Leucine Rich Repeat
TESTI2000644// Small cytokines (intecrine/chemokine),
interleukin-8 like
TESTI2002036// Ion transport protein// Transmembrane region
cyclic Nucleotide Gated Channel
- 25 TESTI2002618// Reprolysin (M12B) family zinc metalloprotease//
Reprolysin family propeptide
TESTI2002928// Syndecan domain
TESTI2003347// Connexin// Cytochrome b559, alpha (gene psbE) and
beta (gene psbF) subunits.
- 30 TESTI2004700// Leucine Rich Repeat// Leucine Rich Repeat//
Leucine Rich Repeat// Leucine Rich Repeat
TESTI2005610// CD36 family
TESTI2006648// Ion transport protein// ABC transporter
transmembrane region.// PEP-utilizing enzymes//
- 35 Phosphoribulokinase// Elongation factor Tu family
TESTI2014716// RNA recognition motif. (a.k.a. RRM, RBD, or RNP

domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 TESTI2024567// 7 transmembrane receptor (metabotropic glutamate
 5 family)
 TESTI2026505// Domain of unknown function DUF123// FYVE zinc
 finger// PH domain// RhoGEF domain
 TESTI2027019// Leucine Rich Repeat
 TESTI2034520// ABC transporter
 10 TESTI2034767// Collagen triple helix repeat (20 copies)//
 Collagen triple helix repeat (20 copies)// Collagen triple helix
 repeat (20 copies)// Collagen triple helix repeat (20 copies)//
 Collagen triple helix repeat (20 copies)// Collagen triple helix
 repeat (20 copies)// Collagen triple helix repeat (20 copies)
 15 TESTI2040018// Hepatitis C virus RNA dependent RNA polymerase
 TESTI2044796// Zinc finger, C3HC4 type (RING finger)
 TESTI2049469// Chitinases class I
 TESTI2050137// Phosphotyrosine interaction domain (PTB/PID)//
 Src homology domain 2
 20 TESTI2050987// Zinc finger, C3HC4 type (RING finger)// SPRY
 domain
 TESTI2051867// Ribosomal protein L4/L1 family
 TESTI2052693// Src homology domain 2
 TESTI2053621// EF hand// EF hand// Glutathione peroxidases// EF
 25 hand
 TESTI4000014// PPR repeat// PPR repeat// PPR repeat// PPR
 repeat// PPR repeat// ENTH domain// PPR repeat// PPR repeat//
 PPR repeat// Ribosomal protein L22p/L17e// Interleukin 10// PPR
 repeat
 30 TESTI4000079// Phosphopantetheine attachment site// PH domain
 TESTI4000288// Dynamin GTPase effector domain
 TESTI4000349// HECT-domain (ubiquitin-transferase).
 TESTI4000462// Keratin, high sulfur B2 protein
 TESTI4000724// Vesicular monoamine transporter// Sugar (and
 35 other) transporter// Monocarboxylate transporter
 TESTI4000970// Ezrin/radixin/moesin family

TESTI4001148// Enol-ase// ATP synthase delta (OSCP) subunit
 TESTI4001527// UDP-glucoronosyl and UDP-glucosyl transferase
 TESTI4001561// Acyltransferase
 TESTI4002491// NSF attachment protein
 5 TESTI4002552// E1-E2 ATPase// Na⁺/K⁺ ATPase C-terminus
 TESTI4006326// von Willebrand factor type A domain
 TESTI4006546// Tudor domain// Tudor domain// Tudor domain
 TESTI4006819// Enol-ase
 TESTI4007064// DENN (AEX-3) domain// PPR repeat// LIM domain
 10 containing proteins
 TESTI4007163// Sodium:neurotransmitter symporter family
 TESTI4007382// Nickel-dependent hydrogenases
 TESTI4007778// Calponin homology (CH) domain// Calponin homology
 (CH) domain// Spectrin repeat// Spectrin repeat// Spectrin
 15 repeat// Spectrin repeat// EF hand// EF hand
 TESTI4007810// DNA ligase
 TESTI4008429// E1-E2 ATPase// Domain of unknown function
 TESTI4009160// Kinesin motor domain// Kinesin motor domain
 TESTI4009374// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 20 domain)// Ham1 family// RNA recognition motif. (a.k.a. RRM, RBD,
 or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// Double-stranded RNA binding motif
 TESTI4009608// emp24/gp25L/p24 family
 TESTI4009881// Bacterial type II secretion system protein
 25 TESTI4010713// C2 domain
 TESTI4010831// WD domain, G-beta repeat
 TESTI4010851// Ubiquitin carboxyl-terminal hydrolases//
 Ubiquitin carboxyl-terminal hydrolase f// eIF4-gamma/eIF5/eIF2-
 epsilon// Rifin/stevor family
 30 TESTI4011484// SAM domain (Sterile alpha motif)
 TESTI4011745// Bromodomain
 TESTI4011956// PH domain
 TESTI4012406// Kringle domain
 TESTI4012448// Matrixin// Hemopexin// Hemopexin// Hemopexin//
 35 Hemopexin
 TESTI4012679// DNA photolyase

TESTI4013369// ATP synthase subunit C
 TESTI4014924// Floricaula / Leafy protein
 TESTI4015471// Tropomyosins
 TESTI4016110// DnaJ domain
 5 TESTI4016882// SH3 domain// SH3 domain
 TESTI4016925// Aminotransferases class-III// Pyridoxal-phosphate
 dependent enzyme
 TESTI4017001// bZIP transcription factor
 TESTI4017137// Keratin, high sulfur B2 protein
 10 TESTI4017575// MSP (Major sperm protein) domain
 TESTI4018152// FERM domain (Band 4.1 family)
 TESTI4018555// Granulins
 TESTI4018835// E1-E2 ATPase// E1-E2 ATPase
 TESTI4018886// Fibronectin type III domain// Fibronectin type
 15 III domain// Fibronectin type III domain
 TESTI4019140// GATA zinc finger
 TESTI4019566// Helicases conserved C-terminal domain// Tudor
 domain
 TESTI4019843// SH3 domain// RhoGEF domain// PH domain
 20 TESTI4020092// Laminin G domain
 TESTI4020920// D-isomer specific 2-hydroxyacid dehydrogenase,
 catalytic domain
 TESTI4021294// Cyclin// Immunoglobulin domain
 TESTI4021478// E1-E2 ATPase// E1-E2 ATPase// E1-E2 ATPase
 25 TESTI4022716// DEAD/DEAH box helicase// Helicases conserved C-
 terminal domain
 TESTI4023555// Lectin C-type domain
 TESTI4025920// Adaptin N terminal region
 TESTI4026192// Domain of unknown function
 30 TESTI4026510// DEAD/DEAH box helicase// Helicases conserved C-
 terminal domain
 TESTI4027557// Vertebrate galactoside-binding lectins//
 Vertebrate galactoside-binding lectins
 TESTI4028059// Phosphofructokinase// Phosphofructokinase
 35 TESTI4028429// WAP-type (Whey Acidic Protein) 'four-disulfide
 core'

- TESTI4028612// Major intrinsic protein
 TESTI4028880// Sugar (and other) transporter//
 Sodium:galactoside symporter family
 TESTI4028983// Serum amyloid A protein
- 5 TESTI4029836// E1-E2 ATPase// E1-E2 ATPase// Neuraxin and MAP1B
 proteins// E1-E2 ATPase// Cof family
 TESTI4030505// Metallothionein family 5
 TESTI4030603// Collagen triple helix repeat (20 copies)
 TESTI4032895// ATP synthase, Delta/Epsilon chain//
- 10 Tropomyosins// Protein of unknown function
 TESTI4034432// Peptidyl-tRNA hydrolase domain
 TESTI4034632// Ribosomal protein S3, C-terminal domain//
 Similarity to lectin domain of ricin beta-chain, 3 copies
 TESTI4034912// Adhesin lipoprotein// Vesiculovirus
- 15 phosphoprotein
 TESTI4035063// Myosin tail// CAP-Gly domain
 TESTI4035498// Cell division protein
 TESTI4036909// Viral (Superfamily 1) RNA helicase// Heavy-metal-
 associated domain// Viral (Superfamily 1) RNA helicase
- 20 TESTI4038492// Serum amyloid A protein
 TESTI4039659// DnaJ domain
 TESTI4041053// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Armadillo/beta-catenin-like repeats// Armadillo/beta-
 catenin-like repeats// Armadillo/beta-catenin-like repeats//
- 25 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// Armadillo/beta-catenin-like repeats
 TESTI4044084// Domain of unknown function
 TESTI4046487// Hantavirus nucleocapsid protein
 TESTI4046819// Metallothionein// PTS HPr component
- 30 phosphorylation sites
 THYMU1000496// Kinesin motor domain
 THYMU2004693// CX module
 THYMU2005303// Immunoglobulin domain
 THYMU2006420// NAD(P) transhydrogenase beta subunit
- 35 THYMU2008725// Similarity to lectin domain of ricin beta-chain,
 3 copies.// Fibronectin type III domain// Fibronectin type III

domain// Fibronectin type III domain// Fibronectin type III
 domain
 THYMU2009425// 7 transmembrane receptor (rhodopsin family)
 THYMU2011548// 7 transmembrane receptor (rhodopsin family)
 5 THYMU2011736// EGF-like domain// EGF-like domain// EB module//
 EGF-like domain// TB domain// EGF-like domain// EGF-like domain
 THYMU2016204// Metallothionein
 THYMU2019210// Class I Histocompatibility antigen, domains alpha
 1 and 2// Class I Histocompatibility antigen, domains alpha 1
 10 and 2// Immunoglobulin domain
 THYMU2023711// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 THYMU2027695// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain// Immunoglobulin domain
 15 THYMU2027734// Parvovirus coat protein VP2
 THYMU2032014// SH3 domain
 THYMU2033079// ABC transporter
 THYMU2035319// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 20 domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 THYMU2035735// FHA domain// SNAP-25 family// Borrelia ORF-A
 THYMU2036459// GTP1/OBG family
 THYMU2037226// SH3 domain// TPR Domain// TPR Domain// TPR
 25 Domain// TPR Domain
 THYMU2038369// Regulatory subunit of type II PKA R-subunit
 THYMU2038615// PH domain
 THYMU2038797// Lectin C-type domain
 THYMU2041015// Sodium:galactoside symporter family// LacY
 30 proton/sugar symporter// Domain of unknown function//
 Monocarboxylate transporter// Polysaccharide biosynthesis
 protein// Sugar (and other) transporter
 THYMU3000028// Zona pellucida-like domain
 THYMU3000133// Viral (Superfamily 1) RNA helicase
 35 THYMU3001234// PH domain
 THYMU3001379// 3'5'-cyclic nucleotide phosphodiesterase//

- Elongation factor Tu family
 THYMU3003212// Cytidine and deoxycytidylate deaminase zinc-binding region
 THYMU3003763// Leucine rich repeat N-terminal domain//
- 5 Polyomavirus coat protein
 THYMU3004835// Galactosyltransferase
 THYMU3006172// C2 domain// C2 domain
 THYMU3007137// PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).
- 10 THYMU3008171// TPR Domain
 THYMU3008436// Phosphofructokinase// Phosphofructokinase
 TLIVE2000023// Integral membrane protein
 TLIVE2002336// Metalloenzyme superfamily// Sulfatase// Type I phosphodiesterase / nucleotide pyrophosphatase
- 15 TLIVE2002338// Transforming growth factor beta like domain
 TLIVE2002690// von Willebrand factor type D domain
 TLIVE2003225// CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)
 TLIVE2003381// 7 transmembrane receptor (metabotropic glutamate family)
- 20 TLIVE2007132// Syndecan domain
 TLIVE2008229// TPR Domain// TPR Domain
 TLIVE2009541// TBC domain
 TRACH2001443// TIR domain
- 25 TRACH2001549// Cyclic nucleotide-binding domain
 TRACH2005811// Kinesin motor domain
 TRACH2006387// NADH-ubiquinone oxidoreductase chain 4, // 7 transmembrane receptor (rhodopsin family)
 TRACH2007059// DnaJ domain// Integrins, beta chain// PA domain
- 30 TRACH2009310// Armadillo/beta-catenin-like repeats// Eukaryotic protein kinase domain// RIO1/ZK632.3/MJ0444 family
 TRACH2019473// Iron/manganese superoxide dismutases (SODM)
 TRACH2021398// RhoGAP domain
 TRACH2022425// Immunoglobulin domain// Subtilase family//
- 35 Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain

- TRACH2022553// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain
- TRACH2022649// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain
- 5 TRACH2023299// Squalene and phytoene synthases// PH domain//
tRNA synthetases class I (E and Q)
TRACH2025535// PH domain
TRACH2025749// Zinc finger, C3HC4 type (RING finger)
TRACH3001427// UBX domain
- 10 TRACH3002168// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain
TRACH3003379// Protein phosphatase 2A regulatory B subunit
TRACH3004786// PMP-22/EMP/MP20/Claudin family
TRACH3004840// Rop protein
- 15 TRACH3005479// Glycosyl transferases group 1
TRACH3005549// Immunoglobulin domain// Immunoglobulin domain
TRACH3006470// Glycosyl transferases group 1
TRACH3007479// WW domain// HECT-domain (ubiquitin-transferase).
TRACH3008093// Putative undecaprenyl diphosphate synthase
- 20 TRACH3008629// Cadherin domain// Cadherin domain// Cadherin
domain// Cadherin domain// Cadherin domain// PQQ enzyme repeat
TRACH3008713// NSF attachment protein
TRACH3009455// Src homology domain 2// FERM domain (Band 4.1
family)// Src homology domain 2
- 25 TRACH3034731// Ras association (RalGDS/AF-6) domain
TRACH3035235// S-100/ICaBP type calcium binding domain
TRACH3035526// Immunoglobulin domain// Cellulose binding
domain// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain
- 30 TRACH3036193// picornavirus capsid protein// Thaumatin family//
Picornavirus core protein 2A// Picornavirus 2B protein//
Extracellular link domain// RNA helicase// 3C cysteine protease
(picornain 3C)// RNA dependent RNA polymerase
TRACH3036609// Immunoglobulin domain
- 35 TSTOM2000442// Immunoglobulin domain// Immunoglobulin domain//
Immunoglobulin domain// Immunoglobulin domain

- TSTOM2000553// C2 domain
 TUTER2000425// KRAB box
 UTERU1000024// NOL1/NOP2/sun family// NOL1/NOP2/sun family
 UTERU1000031// ENTH domain// VHS domain
 5 UTERU1000337// Protein phosphatase 2C
 UTERU2005621// Protein-tyrosine phosphatase// Dual specificity
 phosphatase, catalytic domain
 UTERU2006115// Adaptin N terminal region
 UTERU2006568// IBR domain
 10 UTERU2007724// Calponin homology (CH) domain// Calponin family//
 Calponin family// Calponin family
 UTERU2017762// Ubiquitin family
 UTERU2019706// TCP-1/cpn60 chaperonin family// TCP-1/cpn60
 chaperonin family
 15 UTERU2019940// Ribosomal protein L30p/L7e
 UTERU2025025// Eukaryotic protein kinase domain
 UTERU2026025// RNA recognition motif. (a.k.a. RRM, RBD, or RNP
 domain)
 UTERU2026090// Lectin (probable mannose binding)
 20 UTERU2033375// Ubiquitin carboxyl-terminal hydrolase family 2
 UTERU2035328// WW domain// WW domain// WW domain// FF domain//
 FF domain// FF domain
 UTERU2035331// Fibrillar collagen C-terminal domain
 UTERU2035452// EGF-like domain// Metallothionein// EGF-like
 25 domain
 UTERU2035745// Myosin head (motor domain)// Aldehyde oxidase and
 xanthine dehydrogenase, C terminus
 UTERU2036089// RhoGAP domain
 UTERU2038251// PH domain
 30 UTERU3000645// PMP-22/EMP/MP20/Claudin family
 UTERU3000828// 3'5'-cyclic nucleotide phosphodiesterase//
 Elongation factor Tu family// Elongation factor G C-terminus
 UTERU3001240// Copper/zinc superoxide dismutase (SODC)//
 Adenylate and Guanylate cyclase catalytic domain
 35 UTERU3001585// Cytochrome P450
 UTERU3001652// Wiskott Aldrich syndrome homology region 2

- UTERU3001766// Apidaecin
 UTERU3001988// TPR Domain
 UTERU3002667// Polyomavirus coat protein
 UTERU3002993// NOL1/NOP2/sun family
 5 UTERU3003116// Urease// EGF-like domain
 UTERU3003178// TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// PPR repeat
 UTERU3003523// PH domain// Fibroblast growth factor
 UTERU3004616// Disintegrin
 10 UTERU3004992// Immunoglobulin domain
 UTERU3005460// Penicillin amidase// Bacterial regulatory
 proteins, lacI family
 UTERU3005585// PDZ domain (Also known as DHR or GLGF).
 UTERU3005907// Transglutaminase family
 15 UTERU3006308// Integrins, beta chain// Plexin repeat//
 Immunoglobulin domain
 UTERU3007419// PH domain
 UTERU3007640// NSF attachment protein
 UTERU3008660// TPR Domain// TPR Domain
 20 UTERU3009490// Bromodomain
 UTERU3009871// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// TPR Domain// Ank repeat// Ank repeat
 UTERU3009979// EGF-like domain// EGF-like domain// EGF-like
 domain// Trypsin Inhibitor like cysteine rich domain// EGF-like
 25 domain// Laminin G domain// Thrombospondin N-terminal -like
 domains// Laminin G domain
 UTERU3015500// Leucine rich repeat N-terminal domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 30 Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat

Deduced amino acid sequences of following 250 clones were also detected to have functional domains with Pfam.

- 3NB692004724// KRAB box// Integrase core domain
 35 ADRGL2000042// Nucleosome assembly protein (NAP)
 BLADE2000579// Src homology domain 2// Peptidase family C9

BLADE2006830// HSF-type DNA-binding domain
 BRACE2003609// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 5 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 BRACE2029396// Somatotropin hormone family
 10 BRACE2037299// Integrase core domain
 BRACE2039823// CDP-alcohol phosphatidyltransferase
 BRACE3001058// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 15 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Putative zinc finger in N-recognin//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 factor S-II (TFIIS)// Src homology domain 2// Zinc finger, C2H2
 20 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc
 finger, C2H2 type
 BRACE3001113// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 25 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Putative zinc finger in N-recognin//
 30 Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type
 BRACE3003026// Phorbol esters/diacylglycerol binding domain (C1
 domain)// Zinc finger, C3HC4 type (RING finger)// PHD-finger
 BRACE3003053// Influenza RNA-dependent RNA polymerase subunit//
 Reprolysin family propeptide// Leptin
 35 BRACE3005107// Small cytokines (intecrine/chemokine),
 interleukin-8 like

BRACE3009127// PH domain// Oxysterol-binding protein
 BRACE3010076// KH domain// KH domain// Domain of unknown
 function// KH domain// KH domain// KH domain// Small cytokines
 (intecrine/chemokine), interleukin-8 like// Fanconi anaemia
 5 group C protein// KH domain// KH domain
 BRALZ2017844// Homeobox domain
 BRAMY2019111// Ion transport protein
 BRAMY2035070// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 BRAMY2035449// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 20 C2H2 type// Zinc finger, C2H2 type
 BRAMY2035718// HMG (high mobility group) box// CTF/NF-I family
 BRAMY2038516// Thioredoxin// Thioredoxin
 BRAMY2039341// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 25 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRAMY2040159// Chalcone and stilbene synthases// Adaptor
 complexes medium subunit family// PH domain// Putative GTP-ase
 activating protein for Arf// Ank repeat// Ank repeat
 30 BRAMY2045471// DHHC zinc finger domain
 BRAMY3004800// Synaptobrevin// RhoGEF domain
 BRAWH1000369// DNA polymerase family A
 BRAWH2006207// KRAB box
 BRAWH2006395// Immunoglobulin domain// Thrombospondin type 1
 35 domain
 BRAWH2010552// Cyclin

BRAWH3007441// Zinc finger C-x8-C-x5-C-x3-H type (and similar)
 BRAWH3009017// WD domain, G-beta repeat// WD domain, G-beta
 repeat
 BRCAN2002473// Tropomyosins// Tropomyosins// UvrB/uvrC motif//
 5 Tropomyosins
 BRCAN2002854// SAP domain
 BRCAN2003070// Ubiquitin-conjugating enzyme
 BRCAN2014229// SRP54-type protein// SRP54-type protein//
 Shikimate kinase// Adenylate kinase// ATPases associated with
 10 various cellular activities (AAA)
 BRCOC2019841// Purple acid phosphatase
 BRHIP2005724// alpha/beta hydrolase fold
 BRHIP2006617// TPR Domain// TPR Domain
 BRHIP2008389// Adenylate and Guanylate cyclase catalytic domain
 15 BRHIP2012360// XPG N-terminal domain// XPG I-region
 BRHIP2017553// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 20 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRHIP2026877// Eukaryotic protein kinase domain
 BRHIP3000017// Integrins, beta chain// Uncharacterized protein
 25 family UPF0004
 BRHIP3000240// Aldo/keto reductase family// Aldo/keto reductase
 family
 BRHIP3008314// Sir2 family
 BRHIP3026052// Protein phosphatase 2A regulatory B subunit (B56
 30 family)
 BRSTN2013354// Ets-domain
 BRTHA2002133// Reverse transcriptase (RNA-dependent DNA
 polymerase)
 BRTHA2002702// RNase H
 35 BRTHA2007060// Transposase
 BRTHA2010033// AP endonuclease family 1

BRTHA2013426// AP endonuclease family 1
 BRTHA2013610// Deoxynucleoside kinase
 BRTHA2016318// KE2 family protein
 BRTHA2017364// DEAD/DEAH box helicase// Helicases conserved C-
 5 terminal domain
 BRTHA2017972// Dwarfin
 BRTHA2018011// Trypsin
 BRTHA3000296// Peptidase family M20/M25/M40
 CERVX2002013// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 10 CTONG1000113// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Integrase core domain// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 CTONG2003348// bZIP transcription factor// Importin beta binding
 domain
 20 CTONG2004000// Acyl-CoA dehydrogenase
 CTONG2015596// Myb-like DNA-binding domain
 CTONG2016942// Trypsin
 CTONG2019822// Hepatitis C virus core protein
 CTONG2020374// MORN motif// MORN motif// MORN motif// MORN
 25 motif// MORN motif// MORN motif// MORN motif// Penicillin
 amidase// Bacterial regulatory proteins, lacI family// Vacuolar
 sorting protein 9 (VPS9) domain
 CTONG2020378// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 30 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 CTONG2020411// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 35 CTONG2024031// MORN motif// MORN motif// MORN motif// MORN
 motif// MORN motif// MORN motif// MORN motif// Penicillin

amidase// Bacterial regulatory proteins, lacI family
 CTONG2028758// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Homeobox domain// Zinc finger, C2H2 type// Homeobox domain//
 Zinc finger, C2H2 type

5 CTONG3001501// Zinc finger, C2H2 type
 CTONG3002552// AP endonuclease family 1
 CTONG3003598// AP endonuclease family 1
 CTONG3004550// Phosphoribosyl-ATP pyrophosphohydrolase// Death
 domain

10 CTONG3004726// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type

20 DFNES2011192// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type

FCBBF1000509// SAM domain (Sterile alpha motif)// SURF4 family//

25 SAM domain (Sterile alpha motif)// DNA photolyase
 FCBBF3010361// Fork head domain
 FCBBF3027854// Zinc finger, C2H2 type
 FEBRA2001990// RasGEF domain
 FEBRA2006519// Thrombospondin type 1 domain// Thrombospondin
 30 type 1 domain

FEBRA2008692// PQQ enzyme repeat// wnt family of developmental
 signaling proteins// Eukaryotic protein kinase domain// Ribulose
 biphosphate carboxylase, large chain

FEBRA2014122// Zinc finger, C2H2 type// Zinc finger, C2H2 type//

35 Zinc finger, C2H2 type// Sodium// Zinc finger, C2H2 type
 FEBRA2027609// Zinc finger, C2H2 type// Rubredoxin// Zinc finger,

C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Putative zinc finger in N-
 recognin// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 5 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 FEBRA2028256// EGF-like domain// EGF-like domain// EGF-like
 10 domain// EGF-like domain// EGF-like domain// TB domain// EGF-
 like domain// EGF-like domain// EGF-like domain// EGF-like
 domain// EB module// Squash family of serine protease
 inhibitors// EGF-like domain// EGF-like domain
 FEBRA2028516// GRIP domain
 15 HCASM2002754// Sterol desaturase
 HCASM2003018// PHD-finger// Zinc finger// Zinc finger// Zinc
 finger// Zinc finger// Zinc finger// Zinc finger// Zinc finger//
 Zinc finger// Zinc finger// Zinc finger// Zinc finger// Zinc
 finger
 20 HCASM2003099// Histone deacetylase family// Zn-finger in
 ubiquitin-hydrolases and other proteins
 HCASM2003357// Coproporphyrinogen III oxidase
 HCASM2008536// XRCC1 N terminal domain
 HCASM2009424// RFX DNA-binding domain
 25 HCHON2000508// PH domain// bZIP transcription factor// bZIP
 transcription factor// Outer membrane efflux protein// Troponin
 HCHON2000743// SCAN domain
 HCHON2004858// SCAN domain// Myb-like DNA-binding domain// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 30 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type
 HEART2009680// Bacteriorhodopsin// 7 transmembrane receptor
 35 (Secretin family)
 HLUNG2015418// Cadherin domain// Cadherin domain// Cadherin

domain// Cadherin domain// PQQ enzyme repeat
 HLUNG2015548// IMP dehydrogenase / GMP reductase N terminus//
 CBS domain// CBS domain// Dihydroorotate dehydrogenase//
 Histidine biosynthesis protein// FMN-dependent dehydrogenase//
 5 Conserved region in glutamate synthase// IMP dehydrogenase / GMP
 reductase C terminus
 HSYRA2005628// KRAB box// Zinc finger, C2H2 type// PHD-finger//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 IMR322007078// UBA domain
 IMR322008651// Helix-hairpin-helix motif.
 IMR322013396// Transmembrane region cyclic Nucleotide Gated
 15 Channel// Cyclic nucleotide-binding domain
 IMR322013731// ATPases associated with various cellular
 activities (AAA)// Bromodomain
 LIVER2000247// Sodium
 MESAN2001770// Regulatory subunit of type II PKA R-subunit//
 20 eIF4-gamma/eIF5/eIF2-epsilon
 MESAN2005303// Ank repeat//HECT-domain (ubiquitin-transferase).
 MESAN2014412// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 25 MESAN2015501// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 30 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 35 NT2RI2005772// Guanylate kinase//I/LWEQ domain//PDZ domain (Also
 known as DHR or GLGF).//SH3 domain

- NT2RI2008952// FYVE zinc finger//PHD-finger//Plant PEC family
metallothionein//RNA polymerases M/15 Kd subunits//TRAF-type
zinc finger//Transcription factor S-II (TFIIS)//Zinc finger,
C2H2 type
- 5 NT2RI2009583// 7 transmembrane receptor (metabotropic glutamate
family)//GPR1/FUN34/yaaH family
- NT2RI2018448// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Zinc finger, C2H2 type
- NT2RI2027157// Reeler domain// HSF-type DNA-binding domain
- 10 NT2RI3000174// SNF2 and others N-terminal domain// Small
cytokines (intecrine/chemokine), interleukin-8 like// Helicases
conserved C-terminal domain// Zn-finger in Ran binding protein
and others.// HNH endonuclease
- NT2RI3001132// Zinc finger, C3HC4 type (RING finger)// PHD-
- 15 finger
- NT2RI3002557// Ribosomal protein L36// bZIP transcription factor
- NT2RI3007167// Cold-shock' DNA-binding domain// Zinc knuckle//
Zinc knuckle
- NT2RI3007443// Alpha-2-macroglobulin family// Eukaryotic protein
- 20 kinase domain// REV protein (anti-repression trans-activator
protein)
- NT2RP7008435// Anenome neurotoxin//CUB domain//Low-density
lipoprotein receptor domain class A//Trypsin
- NT2RP8000521// Small cytokines (intecrine/chemokine),
- 25 interleukin-8 like
- NTONG2008093// Adenylylsulfate kinase// 6-phosphofructo-2-kinase
- OCBBF2003327// Thrombospondin type 1 domain// Thrombospondin
type 1 domain// Thrombospondin type 1 domain
- OCBBF2005433// SH3 domain// WW domain// PH domain// RhoGAP
- 30 domain
- OCBBF2006987// Collagen triple helix repeat (20 copies)//
Eukaryotic DNA topoisomerase I
- OCBBF2008144// KRAB box// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 35 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//

Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc
 5 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type
 OCBBF2009583// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type
 OCBBF2011669// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Putative zinc finger in N-recognin//
 Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type
 20 OCBBF2019684// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 25 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 OCBBF2020048// Protein of unknown function DUF98// Zinc finger,
 C3HC4 type (RING finger)
 OCBBF2024284// Hemagglutinin// PHD-finger// Zinc finger// Zinc
 30 finger// Zinc finger// Zinc finger// Zinc finger// Zinc finger//
 Zinc finger// Zinc finger// Zinc finger// Zinc finger// Zinc
 finger// Zinc finger// WD domain, G-beta repeat// WD domain, G-
 beta repeat// WD domain, G-beta repeat
 OCBBF2030116// Hrl repeat motif// Transthyretin precursor
 35 (formerly prealbumin)// Tau and MAP proteins, tubulin-binding//
 Transient receptor// Syntaxin

- OCBBF2032274// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
- 5 OCBBF2034637// Prokaryotic DNA topoisomerase// Protein of
 unknown function// Eukaryotic protein kinase domain
 OCBBF3000167// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
- 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 OCBBF3002654// SH3 domain// Immunoglobulin domain// Eukaryotic
 protein kinase domain
- 15 OCBBF3003761// KH domain// KH domain// Zinc finger, C3HC4 type
 (RING finger)
 PERIC2007068// ELM2 domain// Myb-like DNA-binding domain//
 Eukaryotic initiation factor 1A// Myb-like DNA-binding domain
 PLACE7000333// AP endonuclease family 1
- 20 PLACE7000502// Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Peptidase family C9
 PROST2000452// Trypsin
 PROST2009320// LIM domain containing proteins// LIM domain
 containing proteins
- 25 PUAEN2006335// Formin Homology 2 Domain
 SKMUS2003194// SAP domain
 SPLEN2016135// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Phorbol esters/diacylglycerol binding domain (C1 domain)// Zinc
 finger, C2H2 type
- 30 SPLEN2016781// Transcription factor S-II (TFIIS)// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 SPLEN2030847// Kinesin motor domain// Kinesin motor domain// GGL
 domain
 SPLEN2036702// REJ domain// Phorbol esters/diacylglycerol
 binding domain (C1 domain)// PHD-finger
- 35 SPLEN2039311// dUTPase

SPLEN2039379// Transthyretin precursor (formerly prealbumin)
 STOMA2003158// Deoxyribonuclease I (DNase I)
 SYNOV1000256// Leucine Rich Repeat// BAH domain// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 5 SYNOV2006620// Nuclear transition protein 2
 SYNOV2013637// Chalcone and stilbene synthases
 SYNOV2021953// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 SYNOV4002744// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 SYNOV4003981// Somatomedin B domain// WAP-type (Whey Acidic
 Protein) 'four-disulfide core'// Hemopexin// Hemopexin
 SYNOV4005889// Apolipoprotein A1/A4/E family
 TESOP2000390// Eukaryotic protein kinase domain
 15 TESOP2001796// Zinc finger, C3HC4 type (RING finger)// PHD-
 finger// IBR domain
 TESOP2005199// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-
 20 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc
 finger// Zinc finger, C2H2 type
 TESOP2006398// Zinc finger, C2H2 type
 TESOP2006865// KRAB box
 25 TESTI1000266// Integrase core domain
 TESTI2008901// Transcription factor WhiB
 TESTI2015626// Phosphoribosyl transferase domain
 TESTI2025924// Eukaryotic protein kinase domain
 TESTI2026647// DEAD/DEAH box helicase// Helicases conserved C-
 30 terminal domain
 TESTI2029252// Ion transport protein// Polysaccharide
 biosynthesis protein
 TESTI2034251// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription
 35 factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc

finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

5 TESTI2035981// RNA polymerase alpha subunit
 TESTI2036288// Aldo/keto reductase family
 TESTI2037830// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI2039060// D-ala D-ala ligase// Glycosyl hydrolases family
 31

10 TESTI2049956// WD domain, G-beta repeat// WD domain, G-beta repeat// PQQ enzyme repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

TESTI2050780// Kazal-type serine protease inhibitor domain

15 TESTI4000137// Domain of unknown function
 TESTI4000155// Viral RNA dependent RNA polymerase
 TESTI4000183// KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI4000214// Zinc finger, C3HC4 type (RING finger)// DENN

20 (AEX-3) domain
 TESTI4000319// RasGEF domain
 TESTI4001984// Retroviral aspartyl protease// G-patch domain
 TESTI4005317// Bacterial flagellin C-terminus// Phosphotyrosine interaction domain (PTB/PID)

25 TESTI4006473// Sigma-54 transcription factors// DEAD/DEAH box helicase// DEAD/DEAH box helicase// Ank repeat// Ank repeat// Helicases conserved C-terminal domain
 TESTI4008058// Zn-finger in Ran binding protein and others.// Zinc finger, CCHC class

30 TESTI4008302// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI4010382// Luteovirus (ORF3) RNA-directed RNA-polymerase//

35 Ezrin/radixin/moesin family
 TESTI4011072// Tudor domain// Tudor domain// Staphylococcal

nuclease homologues// Tudor domain// Tudor domain
 TESTI4013365// MYND finger
 TESTI4013894// Synaptophysin / synaptoporin
 TESTI4014801// Zinc finger, C2H2 type// N2,N2-dimethylguanosine
 5 tRNA methyltransferase
 TESTI4015442// Homeobox domain// Zinc finger, C2H2 type//
 Homeobox domain// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 TESTI4017714// Transcriptional regulatory protein, C terminal//
 10 Prolyl oligopeptidase family
 TESTI4021482// Eukaryotic protein kinase domain
 TESTI4024387// GDP dissociation inhibitor
 TESTI4025268// WD domain, G-beta repeat// WD domain, G-beta
 repeat
 15 TESTI4025494// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger,
 20 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI4025547// Type II intron maturase// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI4025865// Lipoate-protein ligase B// KE2 family protein
 25 TESTI4026207// Kinesin motor domain// DNA gyrase/topoisomerase
 IV, subunit A
 TESTI4028938// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 30 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// DM DNA binding domain// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 TESTI4028958// DNA gyrase/topoisomerase IV, subunit A//
 Apolipoprotein A1/A4/E family
 35 TESTI4029348// Trans-activation protein X
 TESTI4029528// RanBP1 domain.

- TESTI4029690// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Cytochrome c oxidase subunit VIa// IQ
 calmodulin-binding motif
- TESTI4031745// Alpha-2-macroglobulin family// Eukaryotic protein
 5 kinase domain// REV protein (anti-repression trans-activator
 protein)
- TESTI4032090// RNase H// Integrase Zinc binding domain//
 Integrase core domain
- TESTI4032112// Syndecan domain
- 10 TESTI4038721// Squash family of serine protease inhibitors
- TESTI4041086// Transmembrane amino acid transporter protein
- TESTI4046240// Sir2 family
- THYMU2004139// Eukaryotic protein kinase domain
- THYMU2004284// Repeat in ubiquitin-activating (UBA) proteins
- 15 THYMU2006001// Zinc finger, C3HC4 type (RING finger)// CONSTANS
 family zinc finger// B-box zinc finger.// SPRY domain
- THYMU2028739// SCAN domain// KRAB box// Myb-like DNA-binding
 domain
- THYMU2031139// Reprolysin (M12B) family zinc metalloprotease//
- 20 Thrombospondin type 1 domain// EB module// Plant PEC family
 metallothionein// A20-like zinc finger
- THYMU2031249// C-type lysozyme/alpha-lactalbumin family//
 Eukaryotic protein kinase domain
- THYMU2035078// Domain of unknown function DUF27
- 25 THYMU2035710// ATP1G1/PLM/MAT8 family
- THYMU2040925// CDP-alcohol phosphatidyltransferase
- THYMU3000269// FAD binding domain
- THYMU3000360// Integrase core domain
- THYMU3001428// Zinc finger, C3HC4 type (RING finger)// PHD-
 30 finger
- TKIDN2012771// DNA polymerase (viral) C-terminal domain// MttB
 family UPF0032
- TLIVE2001684// Alpha-2-macroglobulin family// Alpha-2-
 macroglobulin family
- 35 TLIVE2002046// HMG (high mobility group) box// Uroporphyrinogen
 decarboxylase (URO-D)// Delta-aminolevulinic acid dehydratase

TLIVE2007607// DNA polymerase (viral) C-terminal domain//
 Cytochrome P450
 TRACH1000212// TSC-22/dip/bun family
 TRACH2000862// Guanylate-binding protein
 5 TRACH2007483// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 TRACH2019672// CRAL/TRIO domain.
 TRACH2024408// Death domain
 10 TRACH2024559// IQ calmodulin-binding motif// IQ calmodulin-
 binding motif
 TRACH3000134// KRAB box// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 15 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// DnaJ central domain (4 repeats)// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 20 finger, C2H2 type// Zinc finger, C2H2 type
 TRACH3000420// ABC transporter// Papain family cysteine
 protease// ABC transporter
 TRACH3002561// 'Cold-shock' DNA-binding domain
 TRACH3003832// PHD-finger
 25 TRACH3007866// Transcriptional regulatory protein, C terminal//
 PAC motif// Dipeptidyl peptidase IV (DPP IV) N-terminal region//
 Prolyl oligopeptidase family
 UTERU2004299// ATP P2X receptor
 UTERU2008040// Phorbol esters/diacylglycerol binding domain (C1
 30 domain)// SH3 domain
 UTERU2019534// Cysteine rich repeat// Cysteine rich repeat//
 Carboxylesterases
 UTERU2028734// C2 domain// C2 domain
 UTERU2032279// Serpins (serine protease inhibitors)
 35 UTERU2033577// KRAB box
 UTERU3000402// WD domain, G-beta repeat// WD domain, G-beta

repeat
 UTERU3000738// Eukaryotic protein kinase domain
 UTERU3001053// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 5 C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 UTERU3014791// LIM domain containing proteins// PHD-finger// LIM
 domain containing proteins
 UTERU3015412// WD domain, G-beta repeat// WD domain, G-beta
 10 repeat// WD domain, G-beta repeat// Keratin, high sulfur B2
 protein
 UTERU3017176// K-box region// bZIP transcription factor
 TESTI4038779// K⁺ channel tetramerisation domain// BTB/POZ
 domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 15 Rubredoxin// PHD-finger// Zinc finger, C2H2 type

EXAMPLE 6

Functional categorization based on homology search of the full-length nucleotide sequences and deduced amino acid sequences

20 The functional prediction and categorization of the
 proteins encoded by the clones were carried out based on the
 result of homology search of the databases of GenBank, Swiss-
 Prot, UniGene, nr, and RefSeq (see the Homology Search Result
 Data) for the full-length nucleotide sequences and deduced amino
 25 acid sequences.

A clone predicted to belong to the category of secretory
 protein/membrane protein means a clone having hit data with some
 annotation, such as growth factor, cytokine, hormone, signal,
 transmembrane, membrane, extracellular matrix, receptor, G-
 30 protein coupled receptor, ionic channel, voltage-gated channel,
 calcium channel, cell adhesion, collagen, and connective tissue,
 suggesting that it is a secretory or membrane protein, or means
 a clone in which the presence of nucleotide sequence encoding a
 signal sequence or transmembrane domain was suggested by the
 35 results of PSORT and SOSUI analyses for deduced ORF.

A clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

5 A clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, and SH2 domain, suggesting that the clone encodes a signal transduction-related protein.

10 A clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, and homeobox, suggesting that the clone encodes a transcription-related protein.

15 A clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation and syndrome, suggesting that the clone encodes a disease-related protein, or means a clone whose full-length nucleotide sequence has hit data for
20 Swiss-Prot, GenBank, or UniGene, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database.

25 A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, and E. C. No. (Enzyme commission number), suggesting that the clone encodes an enzyme and/or metabolism-related protein.

30 A clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, and apoptosis, suggesting that the clone encodes a cell division
35 and/or cell proliferation-related protein.

A clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, and microtubules, suggesting that the clone
5 encodes a cytoskeleton-related protein.

A clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, and
10 polyadenylation, suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation,
15 protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, and signal recognition particle, suggesting that the clone encodes a protein synthesis and/or transport-related protein.

A clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, and DNA damage,
20 suggesting that the clone encodes a cellular defense-related protein.

A clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein,
25 suggesting that the clone encodes a development and/or differentiation-related protein.

A clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.
30

A clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

35 In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the

clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional categories in this classification, and there is the possibility that other functions are newly assigned to the protein.

- 5 The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 659 clones.
- ACTVT2000380, ADIPS2000088, ADRGL2000172, ADRGL2003329,
 ADRGL2009146, ASTRO2014923, ASTRO3000301, BLADE1000176,
 BLADE2002073, BLADE2002947, BLADE2004462, BLADE2004670,
 10 BLADE2005036, BLADE2008539, BNGH42003570, BRACE1000186,
 BRACE2005457, BRACE2014306, BRACE2016981, BRACE2029112,
 BRACE2030884, BRACE2031527, BRACE2031531, BRACE2031899,
 BRACE2032385, BRACE2036005, BRACE2039249, BRACE2039327,
 BRACE2040138, BRACE2041200, BRACE2043142, BRACE2043665,
 15 BRACE2046295, BRACE3000697, BRACE3001391, BRACE3002298,
 BRACE3003004, BRACE3003595, BRACE3004058, BRACE3004113,
 BRACE3004772, BRACE3004843, BRACE3006462, BRACE3008137,
 BRACE3008384, BRACE3009574, BRACE3009708, BRACE3010397,
 BRACE3011271, BRACE3011505, BRACE3013740, BRACE3014005,
 20 BRACE3014068, BRACE3014807, BRACE3016884, BRACE3018963,
 BRACE3019084, BRACE3020286, BRACE3020594, BRACE3024662,
 BRACE3025531, BRACE3025630, BRACE3026008, BRACE3026735,
 BRACE3027326, BRACE3031838, BRACE3040856, BRALZ2016085,
 BRAMY2001473, BRAMY2004771, BRAMY2005052, BRAMY2017528,
 25 BRAMY2019300, BRAMY2019963, BRAMY2021498, BRAMY2028856,
 BRAMY2033003, BRAMY2033116, BRAMY2033594, BRAMY2036396,
 BRAMY2039872, BRAMY2040592, BRAMY2041542, BRAMY2045036,
 BRAMY2047420, BRAMY2047751, BRAMY2047765, BRAMY3002312,
 BRAMY3004224, BRAMY3004919, BRAMY3007206, BRAMY3007609,
 30 BRAMY3008505, BRAMY4000095, BRASW1000125, BRAWH1000127,
 BRAWH2002560, BRAWH2002761, BRAWH2007658, BRAWH2014414,
 BRAWH2014954, BRAWH2016221, BRAWH2016439, BRAWH2016702,
 BRAWH3000078, BRAWH3000314, BRAWH3001475, BRAWH3001891,
 BRAWH3002600, BRAWH3003555, BRAWH3003727, BRAWH3003992,
 35 BRAWH3004453, BRAWH3004666, BRAWH3005132, BRAWH3005912,
 BRAWH3006548, BRAWH3007221, BRAWH3007506, BRAWH3007592,

BRAWH3008634, BRCAN2002948, BRCAN2006063, BRCAN2009203,
 BRCAN2010376, BRCAN2012355, BRCAN2012481, BRCAN2013655,
 BRCAN2014143, BRCAN2016619, BRCAN2024451, BRCOC2007034,
 BRCOC2019934, BRHIP2000691, BRHIP2001805, BRHIP2002172,
 5 BRHIP2004814, BRHIP2004883, BRHIP2005236, BRHIP2005752,
 BRHIP2009414, BRHIP2013699, BRHIP2026288, BRHIP3000526,
 BRHIP3007483, BRHIP3007586, BRHIP3008598, BRHIP3009448,
 BRHIP3015751, BRHIP3024118, BRHIP3026097, BRSSN2003086,
 BRSSN2004496, BRSSN2008549, BRSSN2011738, BRSSN2014424,
 10 BRSSN2018925, BRSTN2000872, BRSTN2003835, BRSTN2007000,
 BRSTN2010363, BRSTN2012380, BRSTN2015015, BRSTN2016470,
 BRSTN2016678, BRSTN2017110, BRTHA2002376, BRTHA2002493,
 BRTHA2002608, BRTHA2002808, BRTHA2003110, BRTHA2003461,
 BRTHA2005579, BRTHA2006075, BRTHA2008527, BRTHA2011194,
 15 BRTHA2012980, BRTHA2013460, BRTHA2015696, BRTHA2015878,
 BRTHA2016215, BRTHA2016496, BRTHA2017985, BRTHA2018344,
 BRTHA2018624, BRTHA3000633, BRTHA3002427, BRTHA3003474,
 BRTHA3007148, BRTHA3008386, BRTHA3008778, BRTHA3009037,
 BRTHA3009090, BRTHA3009291, BRTHA3016845, BRTHA3017047,
 20 BRTHA3017589, BRTHA3017848, BRTHA3018656, CERVX2002006,
 COLON2000568, COLON2002443, COLON2004478, COLON2005126,
 COLON2005772, CTONG1000302, CTONG1000341, CTONG1000488,
 CTONG1000508, CTONG2000042, CTONG2004062, CTONG2008233,
 CTONG2009423, CTONG2009531, CTONG2010803, CTONG2013178,
 25 CTONG2019652, CTONG2019788, CTONG2020127, CTONG2020522,
 CTONG2020638, CTONG2022601, CTONG2023512, CTONG2024749,
 CTONG2025496, CTONG2026920, CTONG2027327, CTONG2028124,
 CTONG2028687, CTONG3000707, CTONG3001370, CTONG3001560,
 CTONG3002020, CTONG3003179, CTONG3003483, CTONG3003737,
 30 CTONG3005648, CTONG3008252, CTONG3008258, CTONG3008496,
 CTONG3008566, CTONG3008951, CTONG3009227, CTONG3009239,
 CTONG3009328, CTONG3009385, D3OST2002182, D3OST2002648,
 DFNES1000107, DFNES2000146, DFNES2005266, DFNES2010502,
 FCBBF2001183, FCBBF2007510, FCBBF3003435, FCBBF3004502,
 35 FCBBF3009888, FCBBF3012170, FCBBF3021576, FCBBF3023895,
 FCBBF4000076, FEBRA1000030, FEBRA2007708, FEBRA2008311,

FEBRA2008468, FEBRA2020668, FEBRA2025427, FEBRA2027082,
 HCASM2002502, HCASM2003212, HCASM2007047, HCHON2000212,
 HCHON2001084, HCHON2001548, HCHON2001577, HCHON2001712,
 HCHON2002676, HCHON2004007, HCHON2004776, HCHON2005921,
 5 HEART1000010, HEART2001680, HEART2010492, HLUNG2000014,
 HLUNG2003872, HLUNG2010464, HLUNG2015617, HLUNG2017350,
 HSYRA2005496, HSYRA2006873, HSYRA2008714, HSYRA2009102,
 IMR322002110, IMR322006222, KIDNE1000064, KIDNE2000832,
 KIDNE2000846, KIDNE2006580, KIDNE2010264, KIDNE2011635,
 10 KIDNE2012945, KIDNE2013095, LIVER2007415, LYMPB2000083,
 MESAN2001979, MESAN2012054, MESTC1000042, NHNPC2000606,
 NHNPC2001223, NOVAR2000136, NOVAR2001108, NT2RI2008724,
 NT2RI2009855, NT2RI2025909, NT2RI3001263, NT2RI3003095,
 NT2RI3003382, NT2RI3003409, NT2RI3005403, NT2RI3006171,
 15 NT2RI3006673, NT2RI3007065, NT2RI3007543, NT2RI3007978,
 NT2RP7000359, NT2RP7000466, NT2RP7004027, NT2RP7009030,
 NT2RP7014005, NTONG2000413, OCBBF2006151, OCBBF2006567,
 OCBBF2006764, OCBBF2007114, OCBBF2007428, OCBBF2009926,
 OCBBF2010140, OCBBF2017516, OCBBF2021788, OCBBF2024719,
 20 OCBBF2025458, OCBBF2030517, OCBBF2030574, OCBBF2031167,
 OCBBF2032590, OCBBF2033869, OCBBF2037598, OCBBF2038317,
 OCBBF3000483, OCBBF3003320, OCBBF3004314, PEBLM2000170,
 PEBLM2000338, PEBLM2002594, PEBLM2006113, PEBLM2007834,
 PERIC2001227, PERIC2003452, PERIC2003720, PERIC2004909,
 25 PERIC2005347, PERIC2006035, PERIC2007914, PLACE5000171,
 PLACE5000260, PLACE5000282, PLACE6012574, PLACE6019932,
 PLACE6020031, PLACE7000514, PLACE7001022, PROST1000184,
 PROST1000528, PROST1000559, PROST2003428, PROST2018090,
 PROST2018902, PROST2018922, PUAEN2002489, PUAEN2005588,
 30 PUAEN2006701, PUAEN2009174, PUAEN2009795, RECTM2000433,
 RECTM2001347, SKMUS2000757, SKNMC2002402, SMINT2002743,
 SMINT2009902, SMINT2011888, SMINT2015787, SPLEN2001599,
 SPLEN2009548, SPLEN2012889, SPLEN2015158, SPLEN2015267,
 SPLEN2015679, SPLEN2021701, SPLEN2023733, SPLEN2023791,
 35 SPLEN2025491, SPLEN2029522, SPLEN2029683, SPLEN2030335,
 SPLEN2030479, SPLEN2031125, SPLEN2031424, SPLEN2031547,

SPLEN2031724, SPLEN2031780, SPLEN2032813, SPLEN2033098,
SPLEN2034021, SPLEN2034781, SPLEN2036326, SPLEN2036821,
SPLEN2037722, SPLEN2038180, SPLEN2038345, SPLEN2038407,
SPLEN2040222, SPLEN2041304, SPLEN2042598, STOMA2004294,
5 STOMA2008546, SYNOV2005817, SYNOV2012326, SYNOV2014400,
SYNOV2016124, SYNOV4002883, SYNOV4003322, SYNOV4004184,
SYNOV4004741, SYNOV4004914, SYNOV4006256, SYNOV4007430,
SYNOV4007553, SYNOV4007671, SYNOV4008336, SYNOV4008440,
TBAES2001258, TCERX2000613, TESOP2001345, TESOP2001865,
10 TESOP2002273, TESOP2002539, TESOP2004114, TESOP2005485,
TESOP2005579, TESOP2006041, TESOP2007052, TESOP2007262,
TESOP2007636, TESTI1000257, TESTI1000348, TESTI2000644,
TESTI2002036, TESTI2002618, TESTI2002928, TESTI2003347,
TESTI2005610, TESTI2006648, TESTI2013382, TESTI2024567,
15 TESTI2027019, TESTI2034767, TESTI2034953, TESTI2034997,
TESTI2035997, TESTI2036684, TESTI2042450, TESTI2047071,
TESTI2048898, TESTI2051767, TESTI2052822, TESTI4000215,
TESTI4000724, TESTI4001100, TESTI4001527, TESTI4001561,
TESTI4001665, TESTI4001923, TESTI4002552, TESTI4002754,
20 TESTI4005805, TESTI4005961, TESTI4006053, TESTI4006137,
TESTI4007064, TESTI4007163, TESTI4007239, TESTI4007382,
TESTI4008050, TESTI4008401, TESTI4008429, TESTI4008797,
TESTI4009608, TESTI4012448, TESTI4013369, TESTI4013667,
TESTI4013830, TESTI4014392, TESTI4016238, TESTI4017575,
25 TESTI4017901, TESTI4018835, TESTI4019566, TESTI4020092,
TESTI4020102, TESTI4021478, TESTI4023722, TESTI4024420,
TESTI4024874, TESTI4024890, TESTI4025797, TESTI4026456,
TESTI4026785, TESTI4027821, TESTI4028062, TESTI4028429,
TESTI4028823, TESTI4028880, TESTI4029836, TESTI4030159,
30 TESTI4030505, TESTI4034172, TESTI4035065, TESTI4035649,
TESTI4037244, TESTI4041053, TESTI4042711, TESTI4046487,
TESTI4046819, THYMU2001053, THYMU2003632, THYMU2003760,
THYMU2005003, THYMU2005303, THYMU2005321, THYMU2007658,
THYMU2008725, THYMU2009425, THYMU2011548, THYMU2013386,
35 THYMU2014353, THYMU2019210, THYMU2023711, THYMU2027497,
THYMU2027695, THYMU2029676, THYMU2030068, THYMU2032035,

THYMU2032437, THYMU2032655, THYMU2033079, THYMU2033308,
 THYMU2033816, THYMU2034314, THYMU2035064, THYMU2036085,
 THYMU2036459, THYMU2037226, THYMU2037348, THYMU2038772,
 THYMU2038797, THYMU2039780, THYMU2040412, THYMU2041015,
 5 THYMU3000028, THYMU3000036, THYMU3004835, THYMU3005696,
 THYMU3006168, THYMU3006811, THYMU3007137, THYMU3007368,
 THYMU3007845, TKIDN2002424, TKIDN2002632, TKIDN2006525,
 TKIDN2009092, TKIDN2009889, TKIDN2014771, TKIDN2019116,
 TLIVE2000023, TLIVE2001828, TLIVE2001927, TLIVE2002336,
 10 TLIVE2002690, TLIVE2003381, TLIVE2004110, TLIVE2008229,
 TOVAR2001281, TRACH1000205, TRACH2001549, TRACH2001684,
 TRACH2006387, TRACH2007059, TRACH2007834, TRACH2008300,
 TRACH2020525, TRACH2021964, TRACH2022553, TRACH2025535,
 TRACH2025911, TRACH3000014, TRACH3002064, TRACH3002168,
 15 TRACH3002650, TRACH3004786, TRACH3005294, TRACH3005549,
 TRACH3006149, TRACH3007391, TRACH3008629, TRACH3035199,
 TRACH3035526, TRACH3036193, TSTOM2000442, TSTOM2000553,
 TUTER2000916, UTERU1000339, UTERU2004688, UTERU2004929,
 UTERU2006137, UTERU2006568, UTERU2007444, UTERU2017762,
 20 UTERU2020718, UTERU2022020, UTERU2025025, UTERU2025645,
 UTERU2025891, UTERU2026090, UTERU2026203, UTERU2027591,
 UTERU2029953, UTERU2031851, UTERU2035323, UTERU2035469,
 UTERU3000645, UTERU3000899, UTERU3001240, UTERU3001571,
 UTERU3001585, UTERU3001652, UTERU3001988, UTERU3002209,
 25 UTERU3002383, UTERU3002786, UTERU3003116, UTERU3003776,
 UTERU3006308, UTERU3008671, UTERU3009690, UTERU3009979,
 UTERU3011063, UTERU3015500, UTERU3016789

The following 82 clones are also predicted to belong to the category of secretory protein and/or membrane protein.

30 BLADE2006830, BRACE2002589, BRACE2009318, BRACE2011677,
 BRACE2029396, BRACE2039823, BRACE2039832, BRAMY2019111,
 BRAMY2038516, BRAMY2045471, BRAWH2006395, BRAWH2008993,
 BRCOC2019841, BRHIP2003272, BRHIP2005271, BRHIP2005724,
 BRHIP2008389, BRHIP2026877, BRHIP3000240, BRTHA2011321,
 35 BRTHA2018011, BRTHA2018443, BRTHA3008826, CTONG2015633,
 CTONG2016942, CTONG2019822, FEBRA2000790, FEBRA2006519,

FEBRA2028256, FEBRA2028516, HCASM2002754, HEART2009680,
 HLUNG2013350, HLUNG2015418, IMR322013396, LIVER2000247,
 NT2RI2009583, NT2RI2027157, NT2RP7008435, OCBBF2003327,
 OCBBF2030116, PLACE7000502, PROST2000452, PROST2019487,
 5 SPLEN2016932, SPLEN2037319, SYNOV2001660, SYNOV2013637,
 SYNOV4003981, SYNOV4005889, TBAES2000932, TESTI2015626,
 TESTI2029252, TESTI2032643, TESTI2039060, TESTI2050780,
 TESTI4000137, TESTI4000155, TESTI4006473, TESTI4011070,
 TESTI4013365, TESTI4013894, TESTI4014801, TESTI4032090,
 10 TESTI4041086, THYMU2004284, THYMU2030462, THYMU2033401,
 THYMU2034279, THYMU2035710, THYMU2040925, TKIDN2008778,
 TKIDN2012771, TKIDN2018926, TLIVE2007607, TRACH2019672,
 TRACH3000420, TRACH3003683, UTERU2011220, UTERU2021820,
 UTERU2032279, UTERU3015069

15 The clones predicted to belong to the category of
 glycoprotein-related protein are the following 115 clones.

ADIPS2000088, BNGH42003570, BRACE2005457, BRACE2014306,
 BRACE2029112, BRACE2039249, BRACE2046295, BRACE3001391,
 BRACE3011271, BRACE3016884, BRAMY2005052, BRAMY3004919,
 20 BRAMY4000095, BRAMY4000277, BRAWH1000127, BRAWH2007658,
 BRAWH2014414, BRAWH2016221, BRAWH3002600, BRCAN2006063,
 BRSSN2004496, BRTHA2008527, BRTHA2012980, BRTHA2016496,
 BRTHA3002427, BRTHA3017848, COLON2000568, COLON2004478,
 COLON2005772, CTONG1000341, CTONG2000042, CTONG2009423,
 25 CTONG2023512, CTONG2024749, CTONG2025496, CTONG3001370,
 CTONG3003737, D3OST2002648, DFNES2000146, DFNES2005266,
 FCBBF3012170, FEBRA1000030, FEBRA2008311, FEBRA2008468,
 HCHON2001712, HEART1000010, HEART2001680, HSYRA2005496,
 KIDNE2012945, LYMPB2000083, NESOP2001433, NOVAR2000136,
 30 NOVAR2001108, NT2RI3006171, NT2RI3006673, NT2RP7004027,
 OCBBF2033869, PLACE5000171, PROST1000184, PUAEN2009795,
 SMINT2010076, SMINT2011888, SMINT2015787, SPLEN2015267,
 SPLEN2021701, SPLEN2030335, SYNOV2005817, SYNOV2014400,
 SYNOV3000231, SYNOV3000302, TESOP2004114, TESOP2005485,
 35 TESTI1000257, TESTI2002036, TESTI2002618, TESTI2024567,
 TESTI2027019, TESTI4001527, TESTI4007163, TESTI4012406,

TESTI4013830, TESTI4020092, TESTI4023546, TESTI4028823,
 TESTI4028880, TESTI4046819, THYMU2005303, THYMU2008725,
 THYMU2009425, THYMU2011548, THYMU2019210, THYMU2023711,
 THYMU2027497, THYMU2027695, THYMU2038797, THYMU3004835,
 5 TLIVE2003381, TRACH2006387, TRACH2007059, TRACH2022425,
 TRACH2022553, TRACH2022649, TRACH3002168, TRACH3008629,
 TRACH3035526, TSTOM2000442, UTERU2008347, UTERU2025025,
 UTERU2035469, UTERU3000899, UTERU3001240, UTERU3003116,
 UTERU3006308, UTERU3008671, UTERU3015500

10 The following 15 clones are also predicted to belong to the
 category of glycoprotein-related protein.

BRAMY2019111, BRHIP2026877, BRTHA2018011, FEBRA2028256,
 HEART2009680, HLUNG2015418, NT2RI2009583, NT2RP7008435,
 OCBBF2003327, TESTI2032643, TESTI2039060, TESTI4011070,
 15 THYMU2035710, TRACH3003683, UTERU2032279

The clones predicted to belong to the category of signal
 transduction-related protein are the following 80 clones.

BNGH42007788, BRACE2008594, BRACE2030341, BRACE2044286,
 BRACE3002508, BRACE3003595, BRACE3006872, BRACE3011421,
 20 BRACE3015027, BRACE3027326, BRAMY2036567, BRAMY2038904,
 BRAMY3000213, BRAMY3002803, BRAMY3005091, BRAMY3005932,
 BRAMY4000095, BRAMY4000229, BRCAN2003703, BRCAN2014602,
 BRCAN2016619, BRCAN2028355, BRHIP2000819, BRHIP3025161,
 BRSSN2004719, BRSTN2008418, BRTHA2002281, BRTHA2015406,
 25 CTONG2006798, CTONG3000084, CTONG3002412, D3OST3000169,
 FCBBF3007540, HCASM2001301, HCHON2006250, HCHON2008112,
 HLUNG2002465, KIDNE2001847, NESOP2001694, NT2NE2003252,
 NT2RI2005166, NT2RI3007757, NT2RI3008652, NT2RP7005529,
 NT2RP7009147, NT2RP7013795, NT2RP8000483, OCBBF2004826,
 30 OCBBF2007028, OCBBF2022351, OCBBF2030354, OCBBF2037547,
 PLACE6019385, PLACE7008431, PROST2016462, PROST2018511,
 PUAEN2009852, SPLEN2036932, SYNOV2021320, TESOP2000801,
 TESOP2001166, TESTI2005739, TESTI2026505, TESTI2050137,
 TESTI4011745, TESTI4012505, TESTI4018208, TESTI4028059,
 35 THYMU2007060, THYMU2031046, THYMU2032014, THYMU2039305,

THYMU3008436, TLIVE2001327, TRACH2009310, TRACH2025535,
TRACH3009455, UTERU2025025, UTERU2036089, UTERU3016789

The following 31 clones are also predicted to belong to the category of signal transduction-related protein.

5 BRAMY3004800, BRAWH3009017, BRHIP2026877, BRTHA2013610,
BRTHA2017972, BRTHA3003000, CTONG2020974, FEBRA2001990,
FEBRA2008692, NT2RI2005772, NT2RI3007443, NTONG2008093,
OCBBF2005433, OCBBF2024284, OCBBF2034637, OCBBF3002654,
SPLEN2036702, SPLEN2039379, TESOP2000390, TESTI2025924,
10 TESTI2049956, TESTI4000319, TESTI4019657, TESTI4021482,
TESTI4024387, TESTI4025268, TESTI4031745, THYMU2004139,
THYMU2031249, UTERU2008040, UTERU3000738

The clones predicted to belong to the category of transcription-related protein are the following 38 clones.

15 BRACE2030326, BRACE3001002, BRACE3045033, BRHIP3025161,
BRSSN2014299, BRTHA2014792, BRTHA3001721, CTONG2025516,
FEBRA2007544, FEBRA2007801, HEART1000074, IMR322000127,
IMR322000917, NT2NE2006531, NT2RI2006686, NT2RI3009158,
OCBBF2020838, OCBBF2036743, PEBLM2002887, SKNMC2007504,
20 SPLEN2012624, TESTI2026505, TESTI2040018, TESTI2044796,
TESTI2050987, TESTI4001176, TESTI4007810, TESTI4014175,
TESTI4017543, TESTI4026524, TESTI4036909, THYMU2006420,
THYMU2037233, THYMU3004866, TRACH3000558, TUTER2000425,
UTERU2035328, UTERU3009490

25 The following 64 clones are also predicted to belong to the category of transcription-related protein.

BRACE2003609, BRACE3001058, BRACE3001113, BRALZ2017844,
BRAMY2035070, BRAMY2035449, BRAMY2035718, BRAMY2039341,
BRAWH2006207, BRHIP2017553, CERVX2002013, CTONG1000113,
30 CTONG2003348, CTONG2008721, CTONG2020378, CTONG2020411,
CTONG2028758, CTONG3004726, DFNES2011192, FCBBF3010361,
FEBRA2014122, FEBRA2027609, HCASM2003018, HCHON2004858,
HSYRA2005628, MESAN2005303, MESAN2014412, MESAN2015501,
NT2RI2008952, NT2RI2018448, NT2RI3001132, OCBBF2008144,
35 OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2032274,
OCBBF3000167, SPLEN2004611, SPLEN2016135, SPLEN2016781,

SYNOV2021953, SYNOV4002744, TESOP2001796, TESOP2005199,
 TESOP2006398, TESOP2006865, TESTI2034251, TESTI4000183,
 TESTI4000214, TESTI4008302, TESTI4015442, TESTI4025494,
 TESTI4025547, TESTI4028938, TESTI4032112, THYMU2006001,
 5 THYMU2028739, TRACH2007483, TRACH3000134, TRACH3003832,
 TUTER2000057, UTERU2033577, UTERU3001053, TESTI4038779

The clones predicted to belong to the category of disease-related protein are the following 342 clones.

3NB692002806, ADIPS2000088, BLADE2005036, BRACE2005457,
 10 BRACE2008594, BRACE2014306, BRACE2016981, BRACE2018762,
 BRACE2035381, BRACE2038551, BRACE2039249, BRACE2045300,
 BRACE3000840, BRACE3001002, BRACE3001391, BRACE3001754,
 BRACE3002508, BRACE3003595, BRACE3004058, BRACE3004150,
 BRACE3004772, BRACE3008137, BRACE3008384, BRACE3009708,
 15 BRACE3010397, BRACE3011271, BRACE3011421, BRACE3014807,
 BRACE3015027, BRACE3015521, BRACE3018963, BRACE3020594,
 BRACE3027326, BRALZ2017359, BRAMY2005052, BRAMY2038904,
 BRAMY2047751, BRAMY3000213, BRAMY3005091, BRAMY3007609,
 BRAMY4000095, BRAMY4000229, BRAMY4000277, BRAWH2001395,
 20 BRAWH2002560, BRAWH2010000, BRAWH2010536, BRAWH2014414,
 BRAWH3000100, BRAWH3000491, BRAWH3001326, BRAWH3002574,
 BRAWH3005912, BRAWH3008341, BRCAN2002562, BRCAN2002856,
 BRCAN2002948, BRCAN2003746, BRCAN2006063, BRCAN2009203,
 BRCAN2014602, BRCAN2016619, BRCAN2017442, BRCAN2024451,
 25 BRCOC2001505, BRCOC2003213, BRHIP2000819, BRHIP2001805,
 BRHIP2009414, BRHIP2024165, BRHIP2026288, BRHIP3000339,
 BRHIP3008405, BRHIP3009448, BRHIP3027137, BRHIP3027854,
 BRSSN2000684, BRSSN2004719, BRSSN2014424, BRSTN2001613,
 BRSTN2004987, BRSTN2008418, BRTHA2002608, BRTHA2003110,
 30 BRTHA2007122, BRTHA2007603, BRTHA2008527, BRTHA2012980,
 BRTHA2014792, BRTHA3001721, BRTHA3002427, BRTHA3003074,
 BRTHA3003449, BRTHA3008778, BRTHA3009037, BRTHA3009090,
 BRTHA3015815, BRTHA3016917, BRTHA3017848, COLON2000568,
 COLON2002520, CTONG1000341, CTONG2000042, CTONG2009423,
 35 CTONG2010803, CTONG2017500, CTONG2023021, CTONG2025496,
 CTONG2025516, CTONG3000084, CTONG3002412, CTONG3008639,

D3OST2002182, D3OST2002648, DFNES2001108, FCBBF3009888,
 FEBRA2007708, FEBRA2008468, FEBRA2024744, HCASM2001301,
 HCASM2007737, HCHON2001712, HCHON2002676, HCHON2003532,
 HCHON2004007, HCHON2004531, HCHON2008112, HCHON2008444,
 5 HEART1000010, HEART1000139, HEART2001680, HEART2010495,
 HLUNG2002465, HSYRA2005496, IMR322000127, IMR322001380,
 IMR322006495, KIDNE2001847, KIDNE2012945, NESOP2001694,
 NOVAR2001108, NT2NE2003252, NT2NE2006531, NT2NE2006909,
 NT2RI2006686, NT2RI2025909, NT2RI3001515, NT2RI3006171,
 10 NT2RI3006340, NT2RI3006673, NT2RI3007757, NT2RI3008652,
 NT2RP7000359, NT2RP7005118, NT2RP7005529, NT2RP7010599,
 NTONG2000413, OCBBF2006058, OCBBF2020801, OCBBF2021788,
 OCBBF2031167, OCBBF2033869, OCBBF2036743, OCBBF2037068,
 OCBBF2037340, OCBBF3003320, PEBLM2000170, PEBLM2002887,
 15 PERIC2003720, PERIC2007914, PERIC2008385, PERIC2009086,
 PLACE5000282, PLACE6019385, PROST1000184, PROST2003428,
 PROST2016462, PROST2017367, PROST2018090, PROST2018511,
 PUAEN2002489, PUAEN2009795, SKNMC2007504, SMINT2010076,
 SPLEN2002467, SPLEN2006122, SPLEN2011422, SPLEN2012624,
 20 SPLEN2021701, SPLEN2031547, SPLEN2033098, SPLEN2036326,
 SPLEN2036821, SPLEN2036932, SYNOV2005817, SYNOV2012326,
 SYNOV2014400, SYNOV2021320, SYNOV3000231, SYNOV3000302,
 SYNOV4002883, SYNOV4004741, SYNOV4007360, SYNOV4007521,
 SYNOV4007553, SYNOV4007671, SYNOV4008440, TBAES2001229,
 25 TBAES2001258, TESOP2004114, TESOP2005485, TESOP2009121,
 TESTI1000257, TESTI1000319, TESTI2000644, TESTI2002618,
 TESTI2005610, TESTI2024567, TESTI2026505, TESTI2050987,
 TESTI2051867, TESTI2053399, TESTI2053621, TESTI4000014,
 TESTI4000079, TESTI4000288, TESTI4000349, TESTI4000724,
 30 TESTI4001148, TESTI4001176, TESTI4001527, TESTI4001561,
 TESTI4002491, TESTI4006420, TESTI4006819, TESTI4007163,
 TESTI4007778, TESTI4007810, TESTI4008050, TESTI4008429,
 TESTI4009160, TESTI4009457, TESTI4009881, TESTI4010851,
 TESTI4011745, TESTI4011956, TESTI4012406, TESTI4012448,
 35 TESTI4012505, TESTI4012679, TESTI4013369, TESTI4013924,
 TESTI4014175, TESTI4016110, TESTI4016822, TESTI4016925,

TESTI4017901, TESTI4018835, TESTI4018881, TESTI4018886,
 TESTI4020092, TESTI4021478, TESTI4022873, TESTI4023546,
 TESTI4026524, TESTI4027557, TESTI4028059, TESTI4028429,
 TESTI4028880, TESTI4030069, TESTI4034632, TESTI4034912,
 5 TESTI4035063, TESTI4035498, TESTI4036909, TESTI4037156,
 TESTI4040363, THYMU1000496, THYMU2005303, THYMU2008725,
 THYMU2019210, THYMU2027497, THYMU2027695, THYMU2027734,
 THYMU2031046, THYMU2033104, THYMU2035319, THYMU2037233,
 THYMU2041015, THYMU3001083, THYMU3001234, THYMU3001379,
 10 THYMU3003309, THYMU3004835, THYMU3006118, THYMU3007137,
 THYMU3008436, TKIDN2000701, TKIDN2006852, TLIVE2001327,
 TRACH2001549, TRACH2007059, TRACH2022425, TRACH2022649,
 TRACH3000558, TRACH3002168, TRACH3004721, TRACH3004786,
 TRACH3005549, TRACH3007479, TRACH3008629, TRACH3009455,
 15 TRACH3035526, TSTOM2000442, TUTER2000904, UTERU1000337,
 UTERU2005621, UTERU2007724, UTERU2017762, UTERU2019491,
 UTERU2019706, UTERU2025025, UTERU2026090, UTERU2027591,
 UTERU2035328, UTERU3000645, UTERU3000828, UTERU3000899,
 UTERU3001240, UTERU3001572, UTERU3001585, UTERU3001652,
 20 UTERU3003116, UTERU3003135, UTERU3005907, UTERU3007640,
 UTERU3008671, UTERU3009490, UTERU3009690, UTERU3009979,
 UTERU3015500, UTERU3016789

The following 84 clones are also predicted to belong to the category of disease-related protein.

25 BRACE3001113, BRACE3010076, BRAMY2039341, BRAMY3004800,
 BRAWH3009017, BRCAN2002473, BRCAN2002854, BRCAN2003070,
 BRHIP2005271, BRHIP2017553, BRHIP2026877, BRHIP3000240,
 BRHIP3008314, BRHIP3026052, BRSTN2013354, BRTHA2016318,
 BRTHA2017972, BRTHA3003000, CERVX2002013, CTONG1000113,
 30 CTONG2008721, CTONG2020411, CTONG3004550, FCBBF1000509,
 FEBRA2008692, HCASM2008536, HCHON2004858, HEART2009680,
 HLUNG2015548, HSYRA2005628, IMR322008651, IMR322013396,
 MESAN2001770, NT2RI2009583, NT2RI3007443, OCBBF2003327,
 OCBBF2009583, OCBBF2011669, OCBBF2024284, OCBBF2032274,
 35 OCBBF3000167, OCBBF3002654, PLACE7000502, PROST2000452,
 PROST2009320, SPLEN2004611, STOMA2003158, SYNOV1000256,

SYNOV4002744, SYNOV4003981, TBAES2000932, TESOP2000390,
 TESOP2001796, TESOP2005199, TESTI2015626, TESTI2025924,
 TESTI2026647, TESTI2039060, TESTI4000183, TESTI4006473,
 TESTI4011070, TESTI4017714, TESTI4019657, TESTI4021482,
 5 TESTI4024387, TESTI4025494, TESTI4025547, TESTI4028938,
 TESTI4031745, TESTI4032112, THYMU2004284, THYMU2028739,
 THYMU2031139, THYMU2031249, THYMU2035710, THYMU3000269,
 TLIVE2001684, TLIVE2002046, TRACH2024408, TRACH3003683,
 UTERU2021820, UTERU2032279, UTERU2033577, UTERU3000738

10 In particular, hit data of the following 338 clones for
 Swiss-Prot, or GenBank, UniGene, nr, or RefSeq corresponded to
 genes or proteins which had been deposited in the Online
 Mendelian Inheritance in Man (OMIM), which is the human gene and
 disease database (the OMIM Number is shown in the parenthesis
 15 after the Clone Name).

3NB692002806 (261630), ADIPS2000088 (147120), BLADE2005036
 (114850), BRACE2005457 (274600;603545;600791), BRACE2008594
 (601959), BRACE2014306 (193002), BRACE2016981 (602701),
 BRACE2018762 (604800), BRACE2035381 (606088), BRACE2038551
 20 (601961),
 BRACE2039249 (602273), BRACE2045300 (601442), BRACE3000840
 (600355), BRACE3001002 (300236), BRACE3001391 (601313;173900),
 BRACE3001754 (185641), BRACE3002508 (606417), BRACE3003595
 (602941), BRACE3004058 (250800), BRACE3004150 (601035),
 25 BRACE3004772 (603143), BRACE3008137 (602187), BRACE3008384
 (603264), BRACE3009708 (182340), BRACE3010397 (602187),
 BRACE3011271 (602187), BRACE3011421 (602187), BRACE3014807
 (605784), BRACE3015027 (602187), BRACE3015521 (605888),
 BRACE3018963 (605744), BRACE3020594 (400023), BRACE3027326
 30 (602187), BRALZ2017359 (604331), BRAMY2005052 (602621),
 BRAMY2038904 (605671), BRAMY2047751 (602512), BRAMY3000213
 (605448), BRAMY3005091 (600286), BRAMY3007609 (300315),
 BRAMY4000095 (602187), BRAMY4000229 (602159), BRAMY4000277
 (602187), BRAWH2001395 (159430), BRAWH2002560 (602865),
 35 BRAWH2010000 (602581), BRAWH2010536 (604010), BRAWH2014414
 (603006), BRAWH3000100 (601403), BRAWH3000491 (602187),

BRAWH3001326 (602187), BRAWH3002574 (602187), BRAWH3005912
 (602187), BRAWH3008341 (602187), BRCAN2002562 (602187),
 BRCAN2002856 (602712), BRCAN2002948 (603534), BRCAN2003746
 (311870), BRCAN2006063 (603196;601369), BRCAN2009203 (603143),
 5 BRCAN2014602 (601441), BRCAN2016619 (602187), BRCAN2017442
 (604455), BRCAN2024451 (602513), BRCOC2001505 (159430),
 BRCOC2003213 (602187), BRHIP2000819 (605000), BRHIP2001805
 (603219), BRHIP2009414 (602187), BRHIP2024165 (604402),
 BRHIP2026288 (602187), BRHIP3000339 (159430), BRHIP3008405
 10 (602187), BRHIP3009448 (602187), BRHIP3027137 (600249),
 BRHIP3027854 (601060), BRSSN2000684 (603505), BRSSN2004719
 (600560), BRSSN2014424 (606105), BRSTN2001613 (164020),
 BRSTN2004987 (604733), BRSTN2008418 (602187), BRTHA2002608
 (600463), BRTHA2003110 (602187), BRTHA2007122 (106410),
 15 BRTHA2007603 (605846), BRTHA2008527 (152790;176410),
 BRTHA2012980 (300119), BRTHA2014792 (601674), BRTHA3001721
 (604902),
 BRTHA3002427 (602187), BRTHA3003074 (605367), BRTHA3003449
 (160745), BRTHA3008778 (602187), BRTHA3009037 (602187),
 20 BRTHA3009090 (603197), BRTHA3015815 (600902), BRTHA3016917
 (604137), BRTHA3017848 (603377;212140), COLON2000568 (147000),
 COLON2002520 (602187), CTONG1000341 (188040), CTONG2000042
 (103950), CTONG2009423 (182137), CTONG2010803 (602189),
 CTONG2023021 (602498), CTONG2025496 (103950), CTONG2025516
 25 (601679), CTONG3000084 (600888), CTONG3002412 (601403),
 CTONG3008639 (601797), D3OST2002182 (603590), D3OST2002648
 (603071), DFNES2001108 (603560), FCBBF3009888 (602470),
 FEBRA2007708 (126650;214700), FEBRA2008468 (278000),
 HCASM2001301 (602399), HCASM2007737 (601504), HCHON2001712
 30 (109190),
 HCHON2002676 (252800), HCHON2003532 (172490), HCHON2004007
 (605866), HCHON2004531 (602187), HCHON2008112 (605837),
 HCHON2008444 (602187), HEART1000010 (602187), HEART1000139
 (191045;115195), HEART2001680 (146900), HEART2010495 (157132),
 35 HLUNG2002465 (605216), HSYRA2005496 (131195;187300),
 IMR322000127 (604077), IMR322001380 (605652), IMR322006495

(605607), KIDNE2012945 (600270), NOVAR2001108 (147120),
 NT2NE2003252 (602913), NT2NE2006531 (602277), NT2NE2006909
 (602187),
 NT2RI2006686 (602700), NT2RI2025909 (212138), NT2RI3001515
 5 (300362), NT2RI3006171 (114890), NT2RI3006340 (602187),
 NT2RI3006673 (602187), NT2RI3007757 (605396), NT2RI3008652
 (602654), NT2RP7000359 (603271), NT2RP7005118 (603379),
 NT2RP7005529 (600888), NT2RP7010599 (603684), NTONG2000413
 (602262), OCBBF2006058 (604773), OCBBF2020801 (602187),
 10 OCBBF2021788 (602597), OCBBF2031167 (603709), OCBBF2033869
 (600270), OCBBF2036743 (604075), OCBBF2037068 (602187),
 OCBBF2037340 (602187), OCBBF3003320 (605868), PEBLM2000170
 (602187), PEBLM2002887 (602187), PERIC2003720 (600381),
 PERIC2007914 (400009), PERIC2008385 (604455), PERIC2009086
 15 (600134;605158), PLACE5000282 (130160), PLACE6019385 (602448),
 PROST1000184 (192321), PROST2003428 (602187), PROST2016462
 (602187), PROST2017367 (600585), PROST2018090 (312610),
 PROST2018511 (602187), PUAEN2002489 (604658), PUAEN2009795
 (601456), SKNMC2007504 (602187), SMINT2010076 (146900),
 20 SPLEN2002467 (605652), SPLEN2006122 (604739), SPLEN2011422
 (114213), SPLEN2012624 (602187), SPLEN2021701 (142800),
 SPLEN2031547 (602187), SPLEN2033098 (602746), SPLEN2036326
 (602101), SPLEN2036821 (212138), SPLEN2036932 (605577),
 SYNOV2005817 (123889), SYNOV2012326 (604336), SYNOV2014400
 25 (135820), SYNOV2021320 (602104), SYNOV3000231 (147100),
 SYNOV3000302 (147100), SYNOV4002883 (602187), SYNOV4004741
 (602187), SYNOV4007360 (602187), SYNOV4007521 (605830),
 SYNOV4007553 (603028), SYNOV4007671 (602187), SYNOV4008440
 (602187), TBAES2001229 (602187), TBAES2001258 (142440),
 30 TESOP2004114 (601865), TESOP2005485 (147170), TESOP2009121
 (117143), TESTI1000257 (138170), TESTI1000319 (602187),
 TESTI2000644 (601392), TESTI2002618 (601533), TESTI2005610
 (601040), TESTI2024567 (601116), TESTI2026505 (305400),
 TESTI2050987 (605968), TESTI2051867 (180479), TESTI2053399
 35 (605819), TESTI2053621 (600364;602093), TESTI4000014 (602187),
 TESTI4000079 (603560), TESTI4000288 (602187), TESTI4000349

(604506), TESTI4000724 (603878), TESTI4001148 (602187),
 TESTI4001176 (601430), TESTI4001527 (602187), TESTI4001561
 (602187), TESTI4002491 (602187), TESTI4006420 (605612),
 TESTI4006819 (602187), TESTI4007163 (602187), TESTI4007778
 5 (602187), TESTI4007810 (600940), TESTI4008050 (602187),
 TESTI4008429 (602187), TESTI4009160 (602187), TESTI4009457
 (606185), TESTI4009881 (602187), TESTI4010851 (602187),
 TESTI4011745 (602187), TESTI4011956 (602187), TESTI4012406
 (602187), TESTI4012448 (185261), TESTI4012505 (602143),
 10 TESTI4012679 (601933), TESTI4013369 (602187), TESTI4013924
 (602187), TESTI4014175 (602187), TESTI4016110 (602187),
 TESTI4016822 (601792), TESTI4016925 (602187), TESTI4017901
 (104221), TESTI4018835 (602187), TESTI4018881 (605070),
 TESTI4018886 (602187), TESTI4020092 (156225), TESTI4021478
 15 (605868), TESTI4022873 (602187), TESTI4023546 (602187),
 TESTI4026524 (603277), TESTI4027557 (602187), TESTI4028059
 (232800;171850), TESTI4028429 (602187), TESTI4028880 (138170),
 TESTI4030069 (604603), TESTI4034632 (606251), TESTI4034912
 (602187), TESTI4035063 (602187), TESTI4035498 (602187),
 20 TESTI4036909 (602187), TESTI4037156 (606026), TESTI4040363
 (185641), THYMU1000496 (603060), THYMU2005303 (186910),
 THYMU2008725 (176882), THYMU2019210 (142830), THYMU2027497
 (182139), THYMU2027695 (147100), THYMU2027734 (145505),
 THYMU2031046 (604207), THYMU2033104 (605349), THYMU2035319
 25 (604739), THYMU2037233 (605121), THYMU2041015 (602187),
 THYMU3001083 (602187), THYMU3001234 (602187), THYMU3001379
 (602187), THYMU3003309 (300359), THYMU3004835 (602187),
 THYMU3006118 (603708), THYMU3007137 (602187), THYMU3008436
 (602187), TKIDN2000701 (600465), TKIDN2006852 (603602),
 30 TLIVE2001327 (601403), TRACH2001549 (603197), TRACH2007059
 (602187), TRACH2022425 (146900), TRACH2022649 (147100),
 TRACH3000558 (600140), TRACH3002168 (155735), TRACH3004721
 (602187), TRACH3004786 (602187), TRACH3005549 (602187),
 TRACH3007479 (602308), TRACH3008629 (600976), TRACH3009455
 35 (171833), TRACH3035526 (147000), TSTOM2000442 (147100),
 TUTER2000904 (602187), UTERU1000337 (602187), UTERU2005621

(603505), UTERU2007724 (602373), UTERU2017762 (601053),
 UTERU2019491 (603762), UTERU2019706 (600114), UTERU2025025
 (191315;164970;256000), UTERU2026090 (605497), UTERU2027591
 (600150),
 5 UTERU2035328 (605409), UTERU3000645 (602909), UTERU3000828
 (602187), UTERU3000899 (603062), UTERU3001240 (602187),
 UTERU3001572 (602187), UTERU3001585 (602187), UTERU3001652
 (602715), UTERU3003116 (602187), UTERU3003135 (602187),
 UTERU3005907 (190196), UTERU3007640 (603215), UTERU3008671
 10 (182120), UTERU3009490 (604585), UTERU3009690 (104221),
 UTERU3009979 (600441), UTERU3015500 (606667), UTERU3016789
 (602104)

Additionally, hit data of the following 84 clones for
 Swiss-Prot, or nr or RefSeq corresponded to genes or proteins
 15 which had been deposited in the Online Mendelian Inheritance in
 Man (OMIM), which is the human gene and disease database (the
 OMIM Number is shown in the parenthesis after the Clone Name).

BRACE3001113 (603971), BRACE3010076 (142695), BRAMY2039341
 (604077), BRAMY3004800 (602187), BRAWH3009017 (602187),
 20 BRCAN2002473 (602187), BRCAN2002854 (602895), BRCAN2003070
 (605574), BRHIP2005271 (600267), BRHIP2017553 (602187),
 BRHIP2026877 (600341), BRHIP3000240 (601142), BRHIP3008314
 (604480), BRHIP3026052 (601645), BRSTN2013354 (602187),
 BRTHA2016318 (605442), BRTHA2017972 (602932), BRTHA3003000
 25 (605276), CERVX2002013 (602903), CTONG1000113 (602277),
 CTONG2008721 (605317), CTONG2020411 (601930), CTONG3004550
 (605611), FCBBF1000509 (601933), FEBRA2008692 (604034),
 HCASM2008536 (194360), HCHON2004858 (602187), HEART2009680
 (601970), HLUNG2015548 (146690), HSYRA2005628 (602187),
 30 IMR322008651 (179617), IMR322013396 (600053), MESAN2001770
 (600495), NT2RI2009583 (605949), NT2RI3007443 (602448),
 OCBBF2003327 (605008), OCBBF2009583 (602277), OCBBF2011669
 (602187), OCBBF2024284 (176981), OCBBF2032274 (603975),
 OCBBF3000167 (194558), OCBBF3002654 (601893), PLACE7000502
 35 (164951), PROST2000452 (602060), PROST2009320 (605903),
 SPLEN2004611 (602228), STOMA2003158 (602244), SYNOV1000256

(606021), SYNOV4002744 (602187), SYNOV4003981 (604283),
 TBAES2000932 (606212), TESOP2000390 (602187), TESOP2001796
 (602187), TESOP2005199 (194531), TESTI2015626 (601249),
 TESTI2025924 (600863), TESTI2026647 (601235), TESTI2039060
 5 (154360), TESTI4000183 (601276), TESTI4006473 (602187),
 TESTI4011070 (602187), TESTI4017714 (602187), TESTI4019657
 (602052), TESTI4021482 (164730), TESTI4024387 (602187),
 TESTI4025494 (602187), TESTI4025547 (605308), TESTI4028938
 (603899), TESTI4031745 (602448), TESTI4032112 (603246),
 10 THYMU2004284 (314370), THYMU2028739 (604191), THYMU2031139
 (605009), THYMU2031249 (311550), THYMU2035710 (601890),
 THYMU3000269 (600857), TLIVE2001684 (120700), TLIVE2002046
 (125270), TRACH2024408 (106410), TRACH3003683 (150205),
 UTERU2021820 (126141), UTERU2032279 (600942), UTERU2033577
 15 (603397), UTERU3000738 (602187)

The clones predicted to belong to the category of enzyme
 and/or metabolism-related protein are the following 171 clones.

3NB692002806, ASTRO2002842, BLADE2005036, BRACE2008594,
 BRACE2030341, BRACE2035381, BRACE2038551, BRACE2039249,
 20 BRACE2041200, BRACE2045772, BRACE3004058, BRACE3009708,
 BRACE3011421, BRACE3016884, BRACE3024073, BRACE3025630,
 BRAMY2033267, BRAMY2039872, BRAMY3002803, BRAMY3004919,
 BRAMY3005091, BRAMY3005932, BRAMY4000095, BRAWH3002574,
 BRAWH3008341, BRCAN2003703, BRCAN2003746, BRCAN2009432,
 25 BRCAN2014602, BRCAN2017442, BRCAN2028355, BRCOC2003213,
 BRHIP2024165, BRHIP3008405, BRHIP3027137, BRHIP3027854,
 BRSTN2000872, BRSTN2004863, BRSTN2004987, BRSTN2008418,
 BRTHA2002608, BRTHA2009311, BRTHA2015406, BRTHA2016496,
 BRTHA3008778, BRTHA3009090, BRTHA3015815, BRTHA3016917,
 30 CTONG2004062, CTONG2006798, CTONG2013178, CTONG2028124,
 CTONG3009028, D3OST2002182, DFNES2001108, DFNES2005266,
 FCBBF3013307, FCBBF3023895, FEBRA2008468, FEBRA2026984,
 HCASM2001301, HCHON2002676, HCHON2003532, HCHON2004007,
 HEART2006131, HEART2010492, HHDPC1000118, HLUNG2011298,
 35 HLUNG2013204, HSYRA2008714, KIDNE2001361, KIDNE2006580,
 NT2NE2003252, NT2NE2006909, NT2RI2004618, NT2RI2025909,

NT2RI3006673, NT2RI3007978, NT2RI3008974, NT2RP7000359,
 NT2RP7004027, NT2RP7010599, NT2RP7014005, NTONG2000413,
 NTONG2008672, OCBBF2006005, OCBBF2006058, OCBBF2006151,
 OCBBF2019823, OCBBF2025527, OCBBF2030354, OCBBF2031167,
 5 OCBBF3003320, PEBLM2005183, PERIC2000889, PERIC2008385,
 PLACE6019385, PLACE7008431, PROST2017367, PUAEN2007044,
 PUAEN2009655, PUAEN2009852, SKNMC2006998, SKNMC2007504,
 SMINT1000192, SPLEN2010912, SYNOV2012326, SYNOV4002883,
 TBAES2001258, TESOP2000801, TESOP2004114, TESTI2005610,
 10 TESTI2005739, TESTI2016046, TESTI4000079, TESTI4000209,
 TESTI4000288, TESTI4000349, TESTI4001176, TESTI4001527,
 TESTI4001561, TESTI4002552, TESTI4006148, TESTI4006819,
 TESTI4007810, TESTI4008429, TESTI4010851, TESTI4012406,
 TESTI4012448, TESTI4013369, TESTI4013817, TESTI4014175,
 15 TESTI4016822, TESTI4018152, TESTI4018835, TESTI4019566,
 TESTI4021478, TESTI4022716, TESTI4023546, TESTI4026510,
 TESTI4026524, TESTI4028059, TESTI4029836, TESTI4034632,
 TESTI4036909, TESTI4046819, THYMU2008725, THYMU2027734,
 THYMU2031046, THYMU2031258, THYMU3001234, THYMU3003212,
 20 THYMU3004157, THYMU3004835, THYMU3006118, THYMU3008436,
 TKIDN2006852, TLIVE2002336, TRACH2001549, TRACH2009310,
 TRACH3007479, TRACH3036193, UTERU1000337, UTERU2019491,
 UTERU2025025, UTERU2026203, UTERU3000665, UTERU3001240,
 UTERU3001585, UTERU3003116, UTERU3005907

25 The following 59 clones are also predicted to belong to the
 category of enzyme and/or metabolism-related protein.

BRACE2039823, BRACE3010076, BRAMY2038516, BRAWH1000369,
 BRCAN2003070, BRHIP2005271, BRHIP2012360, BRHIP2026877,
 BRHIP3008314, BRTHA2013610, BRTHA2017364, BRTHA2017972,
 30 BRTHA2018011, BRTHA2018443, BRTHA3003000, CTONG2016942,
 FCBBF1000509, FEBRA2008692, HCASM2003099, HLUNG2015548,
 MESAN2005303, NT2RI3000174, NT2RI3007443, NT2RP7008435,
 NTONG2008093, OCBBF2003327, OCBBF2034637, OCBBF3002654,
 PROST2000452, SPLEN2039311, SPLEN2039379, STOMA2003158,
 35 TESOP2000390, TESTI2015626, TESTI2025924, TESTI2026647,
 TESTI2032643, TESTI2036288, TESTI2039060, TESTI4006473,

TESTI4011070, TESTI4014801, TESTI4017714, TESTI4019657,
 TESTI4021482, TESTI4031745, THYMU2004139, THYMU2004284,
 THYMU2031139, THYMU2031249, THYMU2040925, THYMU3000269,
 TLIVE2002046, TLIVE2007607, TRACH2024559, TRACH3003683,
 5 TRACH3007866, UTERU2021820, UTERU3000738

The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 42 clones.

BLADE2002782, BRACE2042550, BRACE2043248, BRACE3000840,
 10 BRALZ2017359, BRAMY2038484, BRAMY2046989, BRAWH2010536,
 BRAWH2014954, BRAWH3000100, BRHIP2000819, BRHIP2001927,
 BRHIP2009414, BRSSN2000684, CTONG3002412, CTONG3008258,
 CTONG3008639, FCBBF3002163, HCASM2001301, IMR322006495,
 NT2RI2006686, OCBBF2021020, OCBBF2037068, OCBBF3004314,
 15 PLACE5000282, PLACE6019385, PLACE7002641, PUAEN2006328,
 SPLEN2033098, TESOP2009121, TESTI1000545, TESTI2003573,
 TESTI2005610, TESTI4007810, TESTI4017901, THYMU2034374,
 THYMU2039315, TLIVE2001327, TRACH2025507, UTERU2005621,
 UTERU3009690, UTERU3009979

20 The following ten clones are also predicted to belong to the category of cell division and/or cell proliferation-related protein.

BRCAN2003070, BRTHA3003000, NT2RI3007443, PLACE7000502,
 SPLEN2004611, STOMA2003158, SYNOV4003981, TESTI4031745,
 25 THYMU2004139, THYMU2035078

The clones predicted to belong to the category of cytoskeleton-related protein are the following 55 clones.

ASTRO1000009, BLADE2004089, BRACE2026836, BRACE2045300,
 BRACE3006872, BRAMY3008466, BRAWH2001395, BRAWH2005315,
 30 BRAWH3002600, BRCOC2001505, BRHIP2000819, BRHIP3000339,
 BRHIP3008405, BRTHA2007122, BRTHA3003449, COLON2002520,
 CORDB2000541, FCBBF3021940, HCHON2001577, HEART1000139,
 HEART2010495, NT2RI3006340, NT2RP7000359, NTONG2005277,
 OCBBF2007068, OCBBF3003592, PERIC2000889, PLACE5000282,
 35 PROST1000559, SKMUS2006394, SPLEN2011422, SPLEN2015679,
 TESTI2049857, TESTI4000288, TESTI4001148, TESTI4007778,

TESTI4009160, TESTI4009881, TESTI4011956, TESTI4013924,
 TESTI4016925, TESTI4018886, TESTI4022873, TESTI4034912,
 TESTI4035063, TESTI4037727, THYMU1000496, THYMU2035735,
 THYMU3001083, THYMU3001234, TKIDN2000701, UTERU2007724,
 5 UTERU2008347, UTERU2035745, UTERU3003178

The following six clones are also predicted to belong to the category of cytoskeleton-related protein.

HLUNG2015418, SPLEN2030847, SPLEN2036702, TESTI4025268,
 TESTI4026207, TRACH2024408

10 The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 42 clones.

BLADE2007958, BRACE2010489, BRACE2045300, BRACE3004150,
 BRACE3005430, BRACE3011421, BRAMY2046989, BRAMY3005932,
 15 BRCAN2002562, BRHIP2021615, BRSTN2001613, BRSTN2004987,
 COLON2000470, CTONG3009028, FCBBF3013307, HCHON2004531,
 IMR322006495, OCBBF2020801, PEBLM2005183, PUAEN2007044,
 SKNMC1000124, SMINT1000192, SPLEN2006122, SPLEN2010912,
 TESOP2009121, TESTI4009374, TESTI4009457, TESTI4013830,
 20 TESTI4019566, TESTI4022716, THYMU2033104, THYMU2035319,
 THYMU2038301, THYMU2040975, THYMU3001379, TRACH3004721,
 TRACH3036609, UTERU2026025, UTERU3000828, UTERU3001572,
 UTERU3003135, UTERU3004992

25 The following 16 clones are also predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein.

BRACE3010076, BRCAN2002854, BRHIP2006617, BRHIP2012360,
 BRHIP3026052, BRSTN2013354, BRTHA2017364, HCASM2003099,
 HCASM2008536, IMR322008651, NT2RI3000174, STOMA2003158,
 TESTI2026647, TESTI4006473, TESTI4021482, THYMU2035078

30 The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 57 clones.

ASTRO2002842, BLADE2005036, BRACE3025630, BRAMY2033003,
 BRAMY3007609, BRAWH3000491, BRAWH3002574, BRAWH3008341,
 35 BRCAN2002856, BRCAN2002948, BRCOC2003213, BRSTN2004987,
 BRTHA2016496, BRTHA3013884, BRTHA3016917, CTONG2000042,

CTONG2013178, CTONG2023512, CTONG2024749, CTONG2025496,
 CTONG3001370, DFNES2005266, FEBRA2026984, HCASM2007737,
 HCHON2008444, HEART1000010, KIDNE2000846, NT2NE2006909,
 NT2RI2011422, NT2RP7004027, NTONG2000413, OCBBF2031167,
 5 TBAES2001229, TBAES2001258, TESTI1000319, TESTI2005610,
 TESTI2051867, TESTI4000209, TESTI4000349, TESTI4001106,
 TESTI4002491, TESTI4008050, TESTI4010851, TESTI4012406,
 TESTI4012448, TESTI4013924, TESTI4028429, TESTI4034912,
 THYMU2009157, TLIVE2008229, TRACH3007479, TRACH3008713,
 10 TRACH3036193, UTERU2019940, UTERU3001988, UTERU3003116,
 UTERU3007419

The following 15 clones are also predicted to belong to the category of protein synthesis and/or transport-related protein.

BRTHA2007060, BRTHA2018011, CTONG2016942, MESAN2001770,
 15 MESAN2005303, NT2RP7008435, OCBBF2003327, PROST2000452,
 TESOP2001796, TESTI4017714, THYMU2004284, THYMU2031139,
 TRACH2024559, TRACH3007866, UTERU2021820

The clones predicted to belong to the category of cellular defense-related protein are the following three clones.

20 BRACE3005430, HCHON2004531, TESTI4007810

The following four clones are also predicted to belong to the category of cellular defense-related protein.

BRHIP2012360, FCBBF3027854, HCASM2008536, UTERU2032279

The clones predicted to belong to the category of development and/or differentiation-related protein are the following nine clones.

BRACE3009747, BRTHA2005579, BRTHA3003343, IMR322000917,
 PEBLM2000170, TESOP2001122, TESOP2001953, TESTI2040018,
 UTERU3006308

30 The following five clones are also predicted to belong to the category of development and/or differentiation-related protein.

BRALZ2017844, CTONG2020378, HCHON2004858, OCBBF2019684,
 THYMU2006001

35 The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 55 clones.

3NB692002685, BLADE2007958, BRACE2030326, BRACE2045596,
 BRACE3001002, BRACE3004150, BRACE3009747, BRACE3045033,
 BRCAN2002562, BRHIP2021615, BRSSN2014299, BRSTN2001613,
 BRSTN2004987, BRTHA2014792, BRTHA3001721, BRTHA3003343,
 5 CTONG2025516, CTONG3008831, CTONG3009028, FCBBF3013307,
 FEBRA2007544, FEBRA2007801, HEART1000074, IMR322000127,
 IMR322000917, NT2NE2006531, NT2RI3009158, OCBBF2020838,
 OCBBF2036743, PEBLM2002887, PEBLM2005183, SKNMC2007504,
 SMINT1000192, SPLEN2006122, TBAES2001229, TESTI2014716,
 10 TESTI2040018, TESTI2044796, TESTI4009374, TESTI4012679,
 TESTI4014175, TESTI4017543, TESTI4026510, TESTI4026524,
 THYMU2006420, THYMU2035319, THYMU2037233, THYMU2040975,
 THYMU3004866, TLIVE2008229, TRACH3036609, TUTER2000425,
 UTERU2026025, UTERU2035328, UTERU3009490

15 The following 74 clones are also predicted to belong to the
 category of DNA-binding and/or RNA-binding protein.

BRACE2003609, BRACE3001058, BRACE3001113, BRACE3010076,
 BRALZ2017844, BRAMY2035070, BRAMY2035449, BRAMY2035718,
 BRAMY2039341, BRAWH1000369, BRAWH2006207, BRCAN2002854,
 20 BRHIP2012360, BRHIP2017553, BRSTN2013354, BRTHA2017364,
 CERVX2002013, CTONG1000113, CTONG2008721, CTONG2020378,
 CTONG2020411, CTONG2028758, CTONG3004726, DFNES2011192,
 FEBRA2014122, FEBRA2027609, HCASM2003018, HCASM2009424,
 HCHON2004858, HSYRA2005628, IMR322008651, MESAN2001770,
 25 MESAN2005303, MESAN2014412, MESAN2015501, NT2RI2008952,
 NT2RI2018448, NT2RI3000174, NT2RI3001132, OCBBF2008144,
 OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2032274,
 OCBBF3000167, SPLEN2004611, SPLEN2016135, SPLEN2016781,
 SYNOV2021953, SYNOV4002744, TESOP2005199, TESOP2006398,
 30 TESOP2006865, TESTI2026647, TESTI2034251, TESTI4000183,
 TESTI4000214, TESTI4006473, TESTI4008302, TESTI4015442,
 TESTI4025494, TESTI4025547, TESTI4028938, TESTI4032112,
 THYMU2006001, THYMU2035078, TRACH2007483, TRACH3000134,
 TRACH3002561, TRACH3003832, TUTER2000057, UTERU2033577,
 35 UTERU3001053, TESTI4038779

The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 68 clones.

BNGH42007788, BRACE2008594, BRACE2047377, BRACE3005430,
 BRACE3008720, BRACE3009708, BRACE3015521, BRACE3024073,
 5 BRAMY4000095, BRCAN2009432, BRCOC2003213, BRHIP3008405,
 BRSTN2013741, BRTHA3003449, BRTHA3015815, BRTHA3016917,
 COLON2002520, FEBRA2026984, HCASM2001301, HCHON2004007,
 HSYRA2008714, KIDNE2001361, KIDNE2001847, NESOP2001694,
 NT2RI2005166, NT2RP7013795, OCBBF3003320, OCBBF3003592,
 10 PEBLM2002594, PERIC2000889, PLACE6019385, SMINT1000192,
 SPLEN2037194, TESOP2000801, TESTI2006648, TESTI4000288,
 TESTI4001148, TESTI4001176, TESTI4002552, TESTI4007810,
 TESTI4008429, TESTI4009160, TESTI4009881, TESTI4011956,
 TESTI4013817, TESTI4014175, TESTI4016925, TESTI4018208,
 15 TESTI4018835, TESTI4019566, TESTI4021478, TESTI4022873,
 TESTI4026524, TESTI4029836, TESTI4035498, TESTI4036909,
 TESTI4037727, THYMU1000496, THYMU2033079, THYMU3001083,
 THYMU3001234, THYMU3001379, TRACH2009310, UTERU2019706,
 UTERU2025025, UTERU2035745, UTERU3000665, UTERU3000828

20 The following 24 clones are also predicted to belong to the category of ATP binding and/or GTP-binding protein.

BRHIP2026877, BRTHA2017364, BRTHA2018443, IMR322008651,
 IMR322013731, NT2RI3007443, NTONG2008093, OCBBF3002654,
 TESOP2000390, TESOP2007384, TESTI2025924, TESTI2026647,
 25 TESTI2049956, TESTI4005317, TESTI4006473, TESTI4021482,
 TESTI4026207, TESTI4031745, THYMU2004139, THYMU2031249,
 TRACH2000862, TRACH2024559, TRACH3000420, UTERU3000738

The 119 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have
 30 been predicted to have some functions based on homology search using their full-length nucleotide sequences. Clone Name and Definition in the result of homology search, demarcated by a double slash mark (//), are shown below.

ADRGL2009691// Mus musculus D11lgp1 mRNA, complete cds.
 35 ADRGL2009755// Homo sapiens brain and reproductive organ-expressed protein (BRE) mRNA, complete cds.

- ASTRO3000177// *Drosophila melanogaster* BcDNA.GH03694
(BcDNA.GH03694) mRNA, complete cds.
- BLADE2008398// *Homo sapiens* LRR FLI-I interacting protein 2
(LRRFIP2) mRNA, complete cds.
- 5 BRACE2006319// *Homo sapiens* mRNA for Fln29, complete cds.
BRACE2027258// *Homo sapiens* E2a-Pbx1-associated protein (EB-1)
mRNA, partial cds.
BRACE2038329// *Rattus norvegicus* CBL-B (Cbl-b) mRNA, partial cds.
BRACE2046251// *Homo sapiens* hucep-10 mRNA for cerebral protein-
- 10 10, complete cds.
BRACE3003192// latent transforming growth factor beta binding
protein 3 [*Homo sapiens*]
BRACE3007625// *espin* [*Rattus norvegicus*]
BRACE3009297// *mdgl-1* [*Mus musculus*]
- 15 BRACE3015262// *espin* [*Mus musculus*]
BRACE3025457// testis-specific protein TSP-NY [*Homo sapiens*]
BRALZ2016498// *Homo sapiens* FKSG76 (FKSG76) mRNA, complete cds.
BRAMY2030109// *Homo sapiens* hucep-4 mRNA for cerebral protein-4,
complete cds.
- 20 BRAMY2031317// *Mus musculus* semaphorin cytoplasmic domain-
associated protein 3A (Semcap3) mRNA, complete cds.
BRAMY2047746// nasopharyngeal carcinoma susceptibility protein
[*Homo sapiens*]
BRAMY3001794// *Rattus norvegicus* Circadian Oscillatory Protein
- 25 (SCOP) (Scop)
BRAWH2001940// *H.sapiens* gene from PAC 1026E2, partial.
BRAWH2012162// KE03 protein [*Homo sapiens*]
BRAWH2016724// MAP2=HMW-MAP2 {alternatively spliced} [rats,
brain, mRNA Partial, 267 nt].
- 30 BRAWH3002821// synaptotagmin-like 2 [*Mus musculus*]
BRCAN2002944// *Mus musculus* huntington yeast partner C (Hypc)
mRNA, complete cds.
BRCAN2013660// *Arabidopsis thaliana* putative protein (F4F15.330)
mRNA, complete cds.
- 35 BRHIP2002122// *Homo sapiens* B aggressive lymphoma long isoform
(BAL) mRNA, complete cds.

- BRHIP2003786// CCA3 [Rattus norvegicus]
 BRHIP2004359// ELAC PROTEIN.
 BRHIP2007616// plexin 2
 BRHIP2029393// COBW-like protein [Homo sapiens]
 5 BRHIP3008313// testis specific ankyrin-like protein 1 [Homo sapiens]
 BRSSN2013874// TEMO [Rattus norvegicus]
 BRSTN2017771// Homo sapiens putative BTK-binding protein mRNA, complete cds.
 10 BRTHA2012392// Homo sapiens HCDI (HCDI) mRNA, complete cds.
 BRTHA3002933// uroplakin 3 [Homo sapiens]
 BRTHA3008310// Mus musculus mRNA for iroquois homeobox protein 6 (Irx6 gene).
 BRTHA3008520// sporulation-induced transcript 4-associated
 15 protein; hypothetical protein FLJ11058 [Homo sapiens]
 COLON2001721// GLUT4 vesicle protein [Mus musculus]
 CTONG1000467// Mus musculus mRNA for Deltex3, complete cds.
 CTONG2020026// Drosophila melanogaster BcDNA.GH09358 (BcDNA.GH09358) mRNA, complete cds.
 20 CTONG3001123// Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
 CTONG3002127// granuphilin [Mus musculus]
 CTONG3004072// GL002 protein [Homo sapiens]
 CTONG3006186// syntaxin binding protein 4 [Mus musculus]
 25 CTONG3008894// Mus musculus SH3-domain binding protein 5
 FCBBF1000297// Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds.
 HCHON2000028// Homo sapiens 7h3 protein mRNA, partial cds.
 HCHON2000626// X-linked protein STS1769.
 30 HCHON2001217// Homo sapiens cullin CUL4B (CUL4B) mRNA, complete cds.
 HEART2006909// Hemolysin C.
 HLUNG2011041// basic proline-rich peptide IB-8a - human (fragments)
 35 HLUNG2014288// Mus musculus RP42 mRNA, complete cds.
 IMR322006886// Homo sapiens hepatocellular carcinoma-associated

antigen 127 (HCA127) mRNA, complete cds.
 KIDNE2002252// Drosophila melanogaster BcDNA.GH09358
 (BcDNA.GH09358) mRNA, complete cds.
 KIDNE2011532// similar to melanoma-associated chondroitin
 5 sulfate proteoglycan 4
 NT2RI2012990// 76.5 KDA PROTEIN C21ORF13.
 NT2RI2025957// LU1 protein [Homo sapiens]
 NT2RI3006284// Homo sapiens chorea-acanthocytosis (CHAC) mRNA,
 complete cds.
 10 NT2RI3008697// erythroblast macrophage protein [Mus musculus]
 NT2RP8000296// similar to Kelch proteins
 NTONG2007517// RING CANAL PROTEIN (KELCH PROTEIN).
 OCBBF2002124// p40 [Homo sapiens]
 OCBBF2007610// PSD-95/SAP90-associated protein-4 [Rattus
 15 norvegicus].
 OCBBF2021323// Mus musculus GTRGEO22 (Gtrgeo22) mRNA, complete
 cds.
 OCBBF2028173// JM11 protein [Homo sapiens]
 PEBLM2001465// diphthamide biosynthesis; Dph5p [Saccharomyces
 20 cerevisiae]
 PERIC2004028// Mus musculus erythroblast macrophage protein EMP
 mRNA, complete cds.
 PLACE7006051// cytoplasmic dynein heavy chain 2 [Rattus
 norvegicus]
 25 PROST2008993// Mus musculus Pax transcription activation domain
 interacting protein PTIP mRNA, complete cds.
 PUAEN2003079// nasopharyngeal carcinoma susceptibility protein
 [Homo sapiens]
 SPLEN2002147// Halocynthia roretzi mRNA for HrPET-3, complete
 30 cds.
 SPLEN2032154// NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1
 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE
 PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43).
 SYNOV2005216// Homo sapiens laryngeal carcinoma related protein
 35 1 mRNA, complete cds.
 SYNOV2007965// Homo sapiens mRNA for H-1(3)mbt-like protein,

- alternative variant a.
 SYNOV4000706// B cell phosphoinositide 3-kinase adaptor [Mus musculus]
 TBAES2004055// NY-REN-50 antigen
- 5 TESOP2001605// Homo sapiens laryngeal carcinoma related protein 1 mRNA, complete cds.
 TESOP2005285// Homo sapiens partial mRNA for chr2 synaptotagmin (CHR2SYT gene).
 TESTI2004215// Maackia amurensis early nodulin (ENOD2) mRNA,
 10 partial cds.
 TESTI2009477// TRICHOHYALIN.
 TESTI2034520// Rattus norvegicus SMC (segregation of mitotic chromosomes 1)-like 1 (yeast) (Smc1l1), mRNA
 TESTI2052693// brk kinase substrate [Homo sapiens].
- 15 TESTI4006079// MUF1 protein; likely ortholog of mouse MUF1; elongin BC-interacting leucine-rich repeat protein [Homo sapiens]
 TESTI4006393// neural specific sr protein NSSR 2 [Mus musculus]
 TESTI4006546// colon cancer antigen NY-CO-45 [Homo sapiens].
- 20 TESTI4006802// mesothelin; megakaryocyte potentiating factor [Mus musculus]
 TESTI4008018// DAZ associated protein 2; KIAA0058 gene product [Homo sapiens]
 TESTI4009286// Homo sapiens HOTTL protein mRNA, complete cds
- 25 TESTI4009563// testis specific ankyrin-like protein 1 [Homo sapiens]
 TESTI4010831// yeast Sec3lp homolog; ABP125 [Homo sapiens]
 TESTI4011484// Sec23-interacting protein p125 [Homo sapiens]
 TESTI4014818// AD-012 protein [Homo sapiens]
- 30 TESTI4014924// selective hybridizing clone [Mus musculus]
 TESTI4019140// Mi-2 histone deacetylase complex protein 66 [Xenopus laevis]
 TESTI4019843// Rattus norvegicus huntingtin-associated protein interacting protein (duo) (Hapip), mRNA.
- 35 TESTI4023762// Trichohyalin.
 TESTI4025920// B29 protein [Homo sapiens]

- TESTI4039659// DnaJ homolog subfamily B member 8 (mDJ6).
- TESTI4044186// leucine-rich, glioma inactivated 1 [Mus musculus]
- THYMU2011736// latent transforming growth factor beta binding protein 3
- 5 THYMU2032825// Mus musculus mRNA for Drctnnbla, complete cds.
- THYMU2038369// Mus musculus GTRGEO22 (Gtrgeo22) mRNA, complete cds.
- THYMU3001991// ART-4 protein [Homo sapiens]
- THYMU3006172// membrane bound C2 domain containing protein
- 10 [Rattus norvegicus]
- TLIVE2003225// CUB and Sushi multiple domains 1 [Homo sapiens]
- TLIVE2004320// Homo sapiens PC2-glutamine-rich-associated protein (PCQAP) mRNA, complete cds.
- TOVAR2002247// Homo sapiens partial partial mRNA for NICE-4
- 15 protein, clone 3114f17.
- TRACH2023299// growth factor receptor bound protein 2-associated protein 2 [Mus musculus]
- TRACH3000926// cardiac morphogenesis [Mus musculus]
- TRACH3001427// p47 [Homo sapiens]
- 20 TRACH3006412// Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B
- TRACH3034731// Ras association (RalGDS/AF-6) domain family 2
- TUTER2002729// D6MM5E protein [Mus musculus]
- UTERU1000031// G.gallus mRNA for tom-1B protein.
- 25 UTERU2006115// ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).
- UTERU2031268// NY-REN-25 antigen [Homo sapiens].
- UTERU2035452// NG3 [Homo sapiens]
- 30 UTERU3001059// ABC1 protein homolog, mitochondrial precursor.
- UTERU3005585// rhophilin-like protein [Homo sapiens]
- UTERU3009871// feminization 1 homolog a (C. elegans)

Similarly, the 14 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have

35 been predicted to have some functions based on homology search using their full-length nucleotide sequences. Clone Name and

Definition in the result of homology search, demarcated by a double slash mark (//), are shown below.

ADRGL2000042//Homo sapiens CTCL tumor antigen se20-4 mRNA, complete cds.

- 5 BRACE3009127//oxysterol binding protein 2; oxysterol binding protein-like 1 [Homo sapiens]
 BRACE3021148//DC12 protein [Homo sapiens]
 BRAMY2040159//Homo sapiens MRIP-1 mRNA, complete cds.
 BRAWH3007441//CAT56 protein [Homo sapiens]
- 10 CTONG3001501//Mus musculus glucocorticoid-induced gene 1 mRNA, complete cds.
 HCHON2000508//Homo sapiens prostate antigen PARIS-1 mRNA, complete cds.
 OCBBF2020048// 95 kDa retinoblastoma protein binding protein;
- 15 KIAA0661 gene product
 PERIC2007068//Mus musculus mRNA for 1A13 protein.
 TESTI4010382//cytoplasmic dynein heavy chain 2 [Rattus norvegicus]
 TESTI4011072//tudor domain containing 1 [Mus musculus]
- 20 TESTI4046240//sirtuin 7
 UTERU2019534//Golgi apparatus protein 1 [Homo sapiens]
 UTERU2028734//Mus musculus slp2-a mRNA for synaptotagmin-like protein 2-a delta 2S-III, complete cds.

25 So far no information suggesting the function of the remaining 1,061 clones has been provided by the homology search. The functions of these clones may be clarified when an updated database becomes available in future. Clone names are shown below.

- 30 3NB692008729, ADRGL2012038, ADRGL2012179, ASTRO2003960, ASTRO2018373, ASTRO3000172, ASTRO3000482, BLADE2001371, BLADE2001987, BLADE2003474, BLADE2005459, BLADE2007666, BLADE2008281, BRACE1000258, BRACE1000533, BRACE1000572, BRACE2003639, BRACE2011747, BRACE2014475, BRACE2014657, BRACE2015058, BRACE2015314, BRACE2024627, BRACE2027970,
- 35 BRACE2028970, BRACE2029849, BRACE2031154, BRACE2031389, BRACE2032044, BRACE2032329, BRACE2032538, BRACE2032823,

BRACE2033720, BRACE2035441, BRACE2036096, BRACE2036830,
BRACE2036834, BRACE2037847, BRACE2038114, BRACE2039475,
BRACE2039734, BRACE2040325, BRACE2041009, BRACE2041264,
BRACE2043349, BRACE2044816, BRACE2044949, BRACE2045428,
5 BRACE2045947, BRACE2045954, BRACE2047011, BRACE2047350,
BRACE2047385, BRACE3000071, BRACE3000787, BRACE3000973,
BRACE3001217, BRACE3001595, BRACE3002390, BRACE3003698,
BRACE3004358, BRACE3004435, BRACE3004783, BRACE3004880,
BRACE3005145, BRACE3005225, BRACE3005499, BRACE3006185,
10 BRACE3006226, BRACE3007322, BRACE3007472, BRACE3007480,
BRACE3007559, BRACE3007642, BRACE3007767, BRACE3008036,
BRACE3008092, BRACE3008772, BRACE3009090, BRACE3009237,
BRACE3009377, BRACE3009701, BRACE3009724, BRACE3010428,
BRACE3012364, BRACE3012930, BRACE3013119, BRACE3013576,
15 BRACE3013780, BRACE3014231, BRACE3014317, BRACE3015121,
BRACE3015894, BRACE3018308, BRACE3019055, BRACE3020194,
BRACE3022769, BRACE3023912, BRACE3024659, BRACE3025153,
BRACE3026075, BRACE3027242, BRACE3027478, BRACE3030103,
BRACE3032983, BRALZ2011796, BRALZ2012183, BRALZ2012848,
20 BRALZ2014484, BRAMY2003008, BRAMY2019985, BRAMY2020058,
BRAMY2020270, BRAMY2028914, BRAMY2029602, BRAMY2030098,
BRAMY2030702, BRAMY2030703, BRAMY2030799, BRAMY2031377,
BRAMY2031442, BRAMY2032014, BRAMY2032242, BRAMY2032317,
BRAMY2034185, BRAMY2034920, BRAMY2034993, BRAMY2036387,
25 BRAMY2036699, BRAMY2036913, BRAMY2037823, BRAMY2038100,
BRAMY2038846, BRAMY2040478, BRAMY2041261, BRAMY2041378,
BRAMY2042612, BRAMY2042641, BRAMY2042760, BRAMY2042918,
BRAMY2044078, BRAMY2044246, BRAMY2046478, BRAMY2046742,
BRAMY2047169, BRAMY2047676, BRAMY2047884, BRAMY3000206,
30 BRAMY3001401, BRAMY3002620, BRAMY3002805, BRAMY3004672,
BRAMY3004900, BRAMY3006297, BRAMY3008650, BRAMY3009811,
BRAMY3010411, BRASW1000053, BRAWH2001671, BRAWH2001973,
BRAWH2010084, BRAWH2012326, BRAWH2013294, BRAWH2013871,
BRAWH2014645, BRAWH2014662, BRAWH2014876, BRAWH3000345,
35 BRAWH3002819, BRAWH3003522, BRAWH3003801, BRAWH3005422,
BRAWH3005981, BRAWH3006792, BRAWH3007726, BRAWH3007783,

BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2003987,
 BRCAN2004355, BRCAN2005436, BRCAN2006290, BRCAN2006297,
 BRCAN2006450, BRCAN2007144, BRCAN2007409, BRCAN2007426,
 BRCAN2008528, BRCAN2011254, BRCAN2011602, BRCAN2014881,
 5 BRCAN2015371, BRCAN2015464, BRCAN2016433, BRCAN2017717,
 BRCAN2017905, BRCAN2018935, BRCAN2019387, BRCAN2020710,
 BRCAN2021028, BRCAN2024563, BRCAN2025712, BRCOC2000670,
 BRCOC2014033, BRCOC2016525, BRCOC2020142, BRHIP2000826,
 BRHIP2000920, BRHIP2001074, BRHIP2002346, BRHIP2003242,
 10 BRHIP2003917, BRHIP2004312, BRHIP2005354, BRHIP2005600,
 BRHIP2005719, BRHIP2005932, BRHIP2006800, BRHIP2007741,
 BRHIP2009340, BRHIP2009474, BRHIP2014228, BRHIP2022221,
 BRHIP2024146, BRHIP2026061, BRHIP2029176, BRHIP3001283,
 BRHIP3006683, BRHIP3008183, BRHIP3008344, BRHIP3008565,
 15 BRHIP3008997, BRHIP3009099, BRHIP3011241, BRHIP3013765,
 BRHIP3013897, BRHIP3016213, BRHIP3018797, BRHIP3020182,
 BRHIP3024533, BRHIP3024725, BRHIP3025702, BRSSN2006892,
 BRSSN2008797, BRSSN2011262, BRSSN2014556, BRSSN2018581,
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 20 HCHON2000244, HCHON2000418, HCHON2006714, HCHON2007881,
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 HHDPC2001337, HLUNG1000017, HLUNG2001996, HLUNG2002958,
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 25 HLUNG2014449, HLUNG2017546, HLUNG2017806, HLUNG2019058,
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 15 TESOP2006060, TESOP2006068, TESOP2006670, TESOP2006746,
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 30 TESTI4001206, TESTI4002290, TESTI4002647, TESTI4002703,
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5 TESTI4012702, TESTI4013675, TESTI4013685, TESTI4013735,
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10 TESTI4017254, TESTI4017848, TESTI4017961, TESTI4018382,
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30 THYMU2004693, THYMU2005190, THYMU2007179, THYMU2008282,
THYMU2009134, THYMU2016204, THYMU2016523, THYMU2019587,
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THYMU2030226, THYMU2030264, THYMU2030637, THYMU2030796,
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THYMU2038636, THYMU2038739, THYMU2039350, THYMU2039411,
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THYMU3006132, THYMU3006371, THYMU3006485, THYMU3006963,
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10 TKIDN2005934, TKIDN2005947, TKIDN2007667, TKIDN2009641,
TKIDN2010934, TKIDN2012824, TKIDN2013287, TKIDN2014757,
TKIDN2015263, TKIDN2015788, TKIDN2016309, TLIVE2002338,
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TLIVE2006236, TLIVE2006529, TLIVE2007132, TLIVE2007528,
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TRACH2004170, TRACH2005066, TRACH2005811, TRACH2006049,
TRACH2019248, TRACH2019473, TRACH2021398, TRACH2022042,
TRACH2023306, TRACH2025344, TRACH2025749, TRACH2025932,
20 TRACH3000342, TRACH3000586, TRACH3002192, TRACH3002866,
TRACH3002871, TRACH3003379, TRACH3004068, TRACH3004537,
TRACH3004840, TRACH3005479, TRACH3006038, TRACH3006228,
TRACH3006470, TRACH3006889, TRACH3008093, TRACH3008535,
TRACH3034762, TRACH3035235, TRACH3035482, TRACH3036207,
25 TRACH3036309, TRACH3036456, TSTOM1000135, TSTOM2002672,
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UTERU1000249, UTERU2000649, UTERU2001409, UTERU2002410,
UTERU2002841, UTERU2005004, UTERU2007520, UTERU2014678,
UTERU2019681, UTERU2020491, UTERU2021163, UTERU2021380,
30 UTERU2022981, UTERU2023039, UTERU2023175, UTERU2023651,
UTERU2023712, UTERU2024002, UTERU2024656, UTERU2030213,
UTERU2030280, UTERU2031084, UTERU2031521, UTERU2031703,
UTERU2033375, UTERU2033382, UTERU2035114, UTERU2035331,
UTERU2035503, UTERU2037361, UTERU2037577, UTERU2038251,
35 UTERU3000226, UTERU3001542, UTERU3001766, UTERU3002218,
UTERU3002667, UTERU3002731, UTERU3002768, UTERU3002993,

UTERU3003465, UTERU3003523, UTERU3004523, UTERU3004616,
 UTERU3004709, UTERU3005049, UTERU3005205, UTERU3005230,
 UTERU3005460, UTERU3005970, UTERU3006008, UTERU3007134,
 UTERU3007913, UTERU3008660, UTERU3009259, UTERU3009517,
 5 UTERU3015086, UTERU3018081, UTERU3018154, UTERU3018616,
 UTERU3018711

Likewise, so far no information suggesting the function of
 the 72 clones shown below has been provided by the homology
 search. The functions of these clones may be clarified when an
 10 updated database becomes available in future. Clone names are
 shown below.

3NB692004724, ADRGL2000056, BLADE2000579, BRACE2037299,
 BRACE2043105, BRACE3003026, BRACE3003053, BRACE3005107,
 BRACE3015829, BRAMY2041434, BRAWH2009393, BRAWH2010552,
 15 BRCAN2014229, BRHIP2002722, BRHIP3000017, BRTHA2002133,
 BRTHA2002702, BRTHA2010033, BRTHA2013426, BRTHA3000296,
 CTONG2004000, CTONG2015596, CTONG2020374, CTONG2024031,
 CTONG3002552, CTONG3003598, CTONG3009287, HCASM2003357,
 HCHON2000743, HLUNG2016862, IMR322001879, IMR322007078,
 20 NT2RI3002557, NT2RI3005928, NT2RI3007167, NT2RP8000521,
 OCBBF2006987, OCBBF3003761, OCBBF3004972, PLACE7000333,
 PUAEN2006335, SKMUS2003194, SPLEN2033490, STOMA2004893,
 SYNOV2006620, SYNOV4005739, TESTI1000266, TESTI2008901,
 TESTI2035981, TESTI2037830, TESTI4001984, TESTI4008058,
 25 TESTI4011829, TESTI4013602, TESTI4015012, TESTI4025865,
 TESTI4028958, TESTI4029348, TESTI4029528, TESTI4029690,
 TESTI4036767, TESTI4038721, THYMU2032976, THYMU3000360,
 THYMU3001428, TRACH1000212, UTERU2004299, UTERU2035978,
 UTERU3000402, UTERU3014791, UTERU3015412, UTERU3017176

30

EXAMPLE 7

Functional categorization based on a functional domain search for deduced amino acid sequences

Domains and motifs are minimal functional structures of
 35 polypeptides. The structure of a polypeptide is constituted by
 a collection of such minimal structures, and thus the overall

function of a polypeptide is ensured by the resulting structure. Thus, the overall function of a polypeptide can be predicted relatively accurately using data obtained by analysis of domain and motif structures. Furthermore, classifying these results
 5 into functional categories in a database allows clones comprising specific functions to be easily selected. Thus, such databases are highly useful in the functional analysis of each clone.

Pfam was used to undertake a domain search for the amino
 10 acid sequences deduced from the full-length nucleotide sequences (see Example 5). Based on these results, the proteins encoded by clones 664 and 250 were categorized and their functions predicted. This was performed by referring to domain and motif names, accession numbers for hit data, and detailed descriptions
 15 in Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) as well as functional categorizations in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>).

A clone predicted to belong to the category of secretory and/or membrane protein means a clone having domains and motifs,
 20 for example, seven-transmembrane receptor, pancreatic hormone peptides, ion transport protein, or fibroblast growth factor, which suggest receptor, ion channel, hormone, or growth factor.

A clone predicted to belong to the category of glycoprotein-related protein means a clone having domains and
 25 motifs, for example, immunoglobulin domain or glycosyl transferases group 1, which suggest involvement in glycobiology, such as glycoprotein or glycosyltransferase.

A clone predicted to belong to the category of signal transduction-related protein means a clone having domains and
 30 motifs, for example, eukaryotic protein kinase domain, protein phosphatase 2C, or Ras family, which suggest protein kinase, dephosphoenzyme, SH2 domain, or small G protein.

A clone predicted to belong to the category of transcription-related protein means a clone having domains and
 35 motifs, for example, bZIP transcription factor, Zinc finger, or

C2H2 type, which suggest transcription factor or transcription-controlling protein.

5 A clone predicted to belong to the category of disease-related protein means a clone having domains and motifs, for example, Wilm's tumor protein or von Hippel-Lindau disease tumor suppressor protein, which suggest proteins with disease-specific expression or that promote or suppress expression, depending on the disease.

10 A clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having domains and motifs, for example, aldehyde dehydrogenase family, chitin synthase, or glucose-6-phosphate dehydrogenase, which suggest transferase, synthase, or hydrolase.

15 A clone predicted to belong to the category of cell division- and/or cell proliferation-related protein means a clone having domains and motifs, for example, cyclin or cell division protein, which suggest cyclin or cell proliferation-controlling protein.

20 A clone predicted to belong to the category of cytoskeleton-related protein means a clone having domains and motifs, for example, actin, fibronectin type I domain, or kinesin motor domain, which suggest actin, kinesin, or fibronectin.

25 A clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having domains and motifs, for example, hepatitis C virus RNA dependent RNA polymerase or DEAD/DEAH box helicase, which suggest splicing factor, RNA synthase, or helicase.

30 A clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having domains and motifs, for example, translation initiation factor SUI1, ubiquitin family, or ribosomal protein L16, which suggest translation-related protein, ubiquitin-related protein, or ribosomal protein.

35 A clone predicted to belong to the category of cellular defense-related protein means a clone having domains and motifs,

for example, HSP90 protein or DNA mismatch repair protein, which suggest chaperonin or DNA repair protein.

A clone predicted to belong to the category of development- and/or differentiation-related proteins means a clone having
5 domains and motifs, for example, floricaula / leafy protein, which suggest organogenesis-related protein.

A clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having domains and motifs, for example, transcription factor WhiB, B-box zinc finger, or tRNA
10 synthetases class I (C), which suggest DNA/RNA-relating enzyme group including transcription factor and DNA ligase or Zinc-finger related protein.

A clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having domains and motifs, for
15 example, E1-E2 ATPase or Ras family, which suggest ATP/GTP-related enzyme group including ATPase or G protein.

During this functional categorization, if a clone met every criterion of multiple categories as described above, it was grouped into multiple categories. However, the function of a
20 polypeptide is not limited to these functional categories.

The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 64 clones.

ASTRO2014923, ASTRO3000301, BRACE2005457, BRACE2014306,
BRACE3001391, BRACE3014005, BRALZ2016085, BRAMY2040592,
25 BRAWH2014662, BRHIP2004814, BRHIP3024118, BRTHA3002427,
BRTHA3017848, BRTHA3018656, CTONG2009423, CTONG2013178,
D3OST2002648, FEBRA2007708, FEBRA2008311, HCHON2001084,
HCHON2001712, HCHON2004531, HCHON2005921, HSYRA2009102,
KIDNE1000064, KIDNE2000832, NT2RI3006376, OCBBF2031167,
30 OCBBF2035110, OCBBF2038317, PEBLM2002594, PERIC1000147,
PERIC2009086, PROST1000184, SPLEN2012624, SPLEN2031547,
SPLEN2033098, SPLEN2036326, TESTI1000257, TESTI1000390,
TESTI2000644, TESTI2002036, TESTI2002928, TESTI2006648,
TESTI2024567, TESTI2034520, TESTI4000014, TESTI4000724,
35 TESTI4007163, TESTI4009881, TESTI4028880, THYMU2009425,
THYMU2011548, THYMU2033079, THYMU2041015, TLIVE2000023,

TLIVE2003381, TLIVE2007132, TRACH2006387, TRACH2007059,
TRACH3004786, UTERU3000645, UTERU3004616, UTERU3006308

The following 23 clones are also predicted to belong to the category of secretory protein and/or membrane protein.

5 BRACE2029396, BRACE3005107, BRACE3010076, BRAMY2019111,
BRAMY3004800, BRHIP3000017, FCBBF1000509, HCHON2000508,
HEART2009680, IMR322013396, NT2RI2009583, NT2RI3000174,
NT2RP8000521, OCBBF2030116, TESTI2029252, TESTI4013894,
TESTI4032112, TESTI4041086, THYMU2035710, TKIDN2012771,
10 TRACH3000420, UTERU2004299, TESTI4038779

The clones predicted to belong to the category of glycoprotein-related protein are the following 77 clones.

ADIPS2000088, BRACE2043142, BRACE2046295, BRACE3014005,
BRAMY2005052, BRAMY4000277, BRAWH2007658, BRCAN2006063,
15 BRSTN2004863, BRTHA3017589, BRTHA3017848, COLON2000568,
COLON2004478, CTONG2000042, CTONG2013178, CTONG2024206,
CTONG2024749, CTONG2025496, CTONG3001370, CTONG3003737,
D3OST2002182, FEBRA2007708, HCHON2001084, HCHON2002676,
HCHON2004531, HEART2001680, HLUNG2014262, LYMPB2000083,
20 NESOP2001433, NOVAR2001108, NT2RI3006171, NT2RI3006340,
NT2RI3007978, NT2RP7014005, OCBBF2010140, OCBBF2037598,
PLACE5000171, PLACE6012574, PLACE7006051, PUAEN2009174,
SMINT2002743, SMINT2010076, SMINT2011888, SMINT2015787,
SPLEN2001599, SPLEN2015267, SPLEN2021701, SPLEN2037722,
25 STOMA2004294, SYNOV3000231, SYNOV3000302, SYNOV4007521,
SYNOV4007671, TBAES2003550, TESOP2005485, TESTI2005610,
TESTI4006326, TESTI4021294, THYMU2005303, THYMU2019210,
THYMU2023711, THYMU2027695, TRACH2007059, TRACH2022425,
TRACH2022553, TRACH2022649, TRACH3002168, TRACH3005479,
30 TRACH3005549, TRACH3006470, TRACH3035526, TRACH3036609,
TSTOM2000442, UTERU2026090, UTERU3004616, UTERU3004992,
UTERU3006308

The following eight clones are also predicted to belong to the category of glycoprotein-related protein.

35 BRAWH2006395, BRHIP3000017, NT2RI3007443, OCBBF3002654,
TESTI2039060, TESTI4013894, TESTI4031745, TLIVE2001684

The clones predicted to belong to the category of signal transduction-related protein are the following 116 clones.

BLADE2007958, BNGH42007788, BRACE1000258, BRACE2008594,
 BRACE2041009, BRACE3001391, BRACE3006872, BRACE3011421,
 5 BRACE3024073, BRACE3027326, BRALZ2014484, BRAMY2001473,
 BRAMY2036567, BRAMY2042760, BRAMY2047751, BRAMY3001794,
 BRAMY3002803, BRAMY3005091, BRAMY3008466, BRAMY4000095,
 BRAWH3001326, BRAWH3002821, BRAWH3005912, BRCAN2002856,
 BRCAN2009432, BRCAN2016619, BRCAN2024451, BRCAN2028355,
 10 BRHIP2000819, BRHIP2005932, BRHIP3008405, BRHIP3025161,
 BRSSN2000684, BRSSN2004719, BRSTN2008418, BRSTN2013741,
 BRTHA3009037, BRTHA3013884, COLON2001721, CTONG2006798,
 CTONG3000084, CTONG3000657, CTONG3002127, D3OST3000169,
 DFNES2001108, DFNES2011499, FCBBF3007540, HCASM2001301,
 15 HCHON2000028, HCHON2006250, HHDPC1000118, HLUNG2001996,
 HLUNG2002465, KIDNE2001847, MESAN2006563, NHNPC2001816,
 NT2NE2003252, NT2RI2005166, NT2RI3000622, NT2RI3006673,
 NT2RP7005118, NT2RP7005529, NT2RP7009147, NT2RP7013795,
 NT2RP8000483, NTONG2003852, OCBBF2004826, OCBBF2004883,
 20 OCBBF2007028, OCBBF2008770, OCBBF2022351, OCBBF2037340,
 OCBBF2037547, PEBLM2004666, PLACE7008431, PROST2016462,
 PROST2018511, PUAEN2002616, PUAEN2005930, PUAEN2006328,
 PUAEN2009852, SYNOV2021320, TESOP2000801, TESOP2001166,
 TESTI2006648, TESTI2026505, TESTI2050137, TESTI2052693,
 25 TESTI4000079, TESTI4010713, TESTI4010831, TESTI4011956,
 TESTI4016882, TESTI4019843, TESTI4028059, THYMU2032014,
 THYMU2037226, THYMU2038615, THYMU3001234, THYMU3006172,
 THYMU3008436, TLIVE2009541, TRACH2009310, TRACH2021398,
 TRACH2023299, TRACH2025535, TRACH3009455, TRACH3034731,
 30 TSTOM2000553, UTERU1000337, UTERU2005621, UTERU2025025,
 UTERU2036089, UTERU2038251, UTERU3003523, UTERU3007419

The following 38 clones are also predicted to belong to the category of signal transduction-related protein.

BLADE2000579, BRACE3001058, BRACE3003053, BRACE3009127,
 35 BRAMY2040159, BRAMY3004800, BRAWH3009017, BRCAN2014229,
 BRHIP2026877, BRTHA2013610, CTONG3004550, FEBRA2001990,

FEBRA2008692, HCHON2000508, MESAN2001770, NT2RI2005772,
 NT2RI3007443, NTONG2008093, OCBBF2005433, OCBBF2024284,
 OCBBF2034637, OCBBF3002654, TESOP2000390, TESTI2025924,
 TESTI2049956, TESTI4000319, TESTI4005317, TESTI4021482,
 5 TESTI4025268, TESTI4031745, THYMU2004139, THYMU2031249,
 TRACH2024408, UTERU2008040, UTERU2028734, UTERU3000402,
 UTERU3000738, UTERU3015412

The clones predicted to belong to the category of transcription-related protein are the following 27 clones.

10 BRACE2006319, BRACE3013576, BRAMY2030109, BRAWH3005912,
 BRHIP3025161, CORDB1000140, CTONG1000467, HEART2001756,
 IMR322000127, IMR322000917, KIDNE1000064, NOVAR2000136,
 NT2NE2006531, NT2RI3007158, NT2RP7000466, OCBBF2036743,
 OCBBF3009279, PLACE6019385, TESTI2026505, TESTI2044796,
 15 TESTI2050987, TESTI4017001, TESTI4019140, TESTI4034912,
 THYMU2035735, TRACH2025749, TRACH3004840

The following 88 clones are also predicted to belong to the category of transcription-related protein.

BRACE2003609, BRACE3001058, BRACE3001113, BRACE3003026,
 20 BRAMY2035070, BRAMY2035449, BRAMY2035718, BRAMY2039341,
 BRAMY2045471, BRAWH3007441, BRHIP2017553, BRSTN2013354,
 CERVX2002013, CTONG1000113, CTONG2003348, CTONG2020374,
 CTONG2020378, CTONG2020411, CTONG2024031, CTONG2028758,
 CTONG3001501, CTONG3004726, DFNES2011192, FCBBF3027854,
 25 FEBRA2014122, FEBRA2027609, HCASM2003018, HCASM2003099,
 HCHON2000508, HCHON2000743, HCHON2004858, HSYRA2005628,
 MESAN2014412, MESAN2015501, NT2RI2008952, NT2RI2018448,
 NT2RI3000174, NT2RI3001132, NT2RI3002557, NT2RI3007167,
 NT2RI3007443, OCBBF2008144, OCBBF2009583, OCBBF2011669,
 30 OCBBF2019684, OCBBF2020048, OCBBF2024284, OCBBF2032274,
 OCBBF3000167, OCBBF3003761, SPLEN2016135, SPLEN2016781,
 SPLEN2036702, SYNOV2021953, SYNOV4002744, TESOP2001796,
 TESOP2005199, TESOP2006398, TESTI2008901, TESTI2034251,
 TESTI2037830, TESTI4000183, TESTI4000214, TESTI4006473,
 35 TESTI4008058, TESTI4008302, TESTI4013365, TESTI4014801,
 TESTI4015442, TESTI4017714, TESTI4025494, TESTI4025547,

TESTI4028938, TESTI4029348, TESTI4031745, TESTI4032090,
 THYMU2006001, THYMU2028739, THYMU2031139, THYMU3001428,
 TRACH2007483, TRACH3000134, TRACH3003832, TRACH3007866,
 UTERU3001053, UTERU3014791, UTERU3017176, TESTI4038779

5 The clones predicted to belong to the category of enzyme
 and/or metabolism-related protein are the following 176 clones.

3NB692002806, ASTRO1000009, BLADE2005036, BLADE2008539,
 BRACE2005457, BRACE2008594, BRACE2014475, BRACE2018762,
 BRACE2035381, BRACE2043142, BRACE2047011, BRACE3004058,
 10 BRACE3007625, BRACE3009708, BRACE3011421, BRACE3015262,
 BRACE3024073, BRACE3025630, BRACE3027478, BRAMY2047746,
 BRAMY2047751, BRAMY3002803, BRAMY3004919, BRAMY3005091,
 BRAMY4000095, BRAWH2010000, BRAWH2014414, BRAWH2014662,
 BRAWH2016702, BRAWH3002821, BRAWH3003727, BRCAN2021028,
 15 BRCAN2024451, BRCAN2028355, BRCOC2003213, BRHIP2004359,
 BRHIP2026288, BRHIP3008183, BRHIP3025161, BRHIP3027137,
 BRSSN2000684, BRSTN2000872, BRSTN2004863, BRSTN2004987,
 BRTHA2012980, BRTHA3002401, BRTHA3008778, BRTHA3009037,
 BRTHA3009090, BRTHA3015815, BRTHA3016917, BRTHA3017848,
 20 BRTHA3018656, COLON2001721, CTONG2004062, CTONG2006798,
 CTONG2013178, CTONG2028124, CTONG3002127, CTONG3005325,
 CTONG3005648, D3OST2002182, FCBBF3004502, FCBBF3013307,
 FEBRA2007708, FEBRA2008468, FEBRA2026984, HCASM2001301,
 HCASM2002918, HCHON2002676, HCHON2004007, HCHON2004531,
 25 HEART2006131, HHDPC1000118, HLUNG1000017, KIDNE2000832,
 KIDNE2006580, MESAN2012054, NOVAR2000136, NT2NE2003252,
 NT2NE2006909, NT2RI2004618, NT2RI3004510, NT2RI3006673,
 NT2RI3007978, NT2RI3008652, NT2RP7010599, NT2RP7014005,
 NT2RP7017474, NTONG2000413, OCBBF2004826, OCBBF2006058,
 30 OCBBF2019823, OCBBF2025527, OCBBF2031167, OCBBF2037340,
 OCBBF2037547, OCBBF2037638, PERIC2009086, PLACE7002641,
 PLACE7008431, PROST2017367, PUAEN2007044, PUAEN2009795,
 PUAEN2009852, SPLEN2010912, SPLEN2015679, SPLEN2030335,
 SYNOV4002392, SYNOV4002883, TBAES2003550, TESOP2000801,
 35 TESOP2004114, TESOP2009121, TESTI1000257, TESTI1000545,
 TESTI2002618, TESTI2006648, TESTI2040018, TESTI2049469,

TESTI2053621, TESTI4000288, TESTI4000349, TESTI4001148,
 TESTI4001527, TESTI4001561, TESTI4002552, TESTI4006819,
 TESTI4007382, TESTI4007810, TESTI4008429, TESTI4010713,
 TESTI4010851, TESTI4012448, TESTI4012679, TESTI4013369,
 5 TESTI4016925, TESTI4018835, TESTI4020920, TESTI4021478,
 TESTI4022716, TESTI4026510, TESTI4028059, TESTI4029836,
 TESTI4032895, TESTI4034432, TESTI4036909, THYMU2006420,
 THYMU3000133, THYMU3001379, THYMU3004835, THYMU3006172,
 THYMU3008436, TLIVE2002336, TRACH2006387, TRACH2009310,
 10 TRACH2019473, TRACH2022425, TRACH2023299, TRACH3005479,
 TRACH3006470, TRACH3007479, TRACH3008093, TRACH3008629,
 TRACH3036193, TSTOM2000553, UTERU2005621, UTERU2017762,
 UTERU2025025, UTERU2033375, UTERU3000828, UTERU3001240,
 UTERU3001585, UTERU3003116, UTERU3005460, UTERU3005907
 15 The following 89 clones are also predicted to belong to the
 category of enzyme and/or metabolism-related protein.
 BLADE2000579, BRACE2039823, BRACE3003053, BRAMY2038516,
 BRAMY2040159, BRAWH1000369, BRCAN2003070, BRCAN2014229,
 BRCOC2019841, BRHIP2005724, BRHIP2008389, BRHIP2026877,
 20 BRHIP3000240, BRHIP3026052, BRTHA2002133, BRTHA2002702,
 BRTHA2007060, BRTHA2010033, BRTHA2013426, BRTHA2013610,
 BRTHA2017364, BRTHA2018011, BRTHA3000296, CTONG2004000,
 CTONG2016942, CTONG2020374, CTONG2024031, CTONG3002552,
 CTONG3003598, CTONG3004550, FCBBF1000509, FEBRA2008692,
 25 HCASM2002754, HCASM2003099, HCASM2003357, HLUNG2015418,
 HLUNG2015548, IMR322013731, MESAN2005303, NT2RI2005772,
 NT2RI2008952, NT2RI3000174, NT2RI3007443, NT2RP7008435,
 NTONG2008093, OCBBF2006987, OCBBF2034637, OCBBF3002654,
 PLACE7000333, PLACE7000502, PROST2000452, SPLEN2039311,
 30 STOMA2003158, SYNOV2013637, TESOP2000390, TESTI2015626,
 TESTI2025924, TESTI2026647, TESTI2035981, TESTI2036288,
 TESTI2039060, TESTI2049956, TESTI4000155, TESTI4001984,
 TESTI4006473, TESTI4010382, TESTI4011072, TESTI4014801,
 TESTI4017714, TESTI4021482, TESTI4025547, TESTI4025865,
 35 TESTI4026207, TESTI4028958, TESTI4029690, TESTI4031745,
 TESTI4032090, THYMU2004139, THYMU2031139, THYMU2031249,

THYMU2040925, TKIDN2012771, TLIVE2002046, TLIVE2007607,
 TRACH3000420, TRACH3007866, UTERU2019534, UTERU2028734,
 UTERU3000738

5 The clones predicted to belong to the category of cell
 division and/or cell proliferation-related protein are the
 following ten clones.

BRAWH2001940, CTONG3001123, HCHON2001217, PROST2008993,
 TBAES2001171, TESTI4021294, TESTI4035498, UTERU1000024,
 UTERU3002993, UTERU3003523

10 The following three clones are also predicted to belong to
 the category of cell division and/or cell proliferation-related
 protein.

BRACE2029396, BRAWH2010552, TESTI4013365.

15 The clones predicted to belong to the category of
 cytoskeleton-related protein are the following 36 clones.

BRACE2026836, BRACE2045300, BRAWH3000314, BRSTN2004863,
 BRTHA2004978, BRTHA3003449, BRTHA3005046, COLON2002520,
 CORDB2000541, CTONG3002674, FCBBF3012288, HCHON2001577,
 HLUNG2017350, HSYRA2005456, HSYRA2009075, NT2RI3006340,
 20 NT2RI3006673, NT2RI3007291, OCBBF2037598, PLACE5000282,
 TESTI2003347, TESTI2034767, TESTI4000288, TESTI4007778,
 TESTI4009160, TESTI4018886, TESTI4030603, TESTI4034632,
 TESTI4035063, THYMU1000496, THYMU2008725, TRACH2005811,
 TRACH2007059, UTERU2007724, UTERU2035745, UTERU3004616

25 The following four clones are also predicted to belong to
 the category of cytoskeleton-related protein.

NT2RI2005772, OCBBF2006987, SPLEN2030847, TESTI4026207

30 The clones predicted to belong to the category of nuclear
 protein and/or RNA synthesis-related protein are the following
 20 clones.

BRACE3024073, BRAWH2001940, BRCOC2003213, BRSTN2004987,
 BRTHA3016917, CTONG3009028, FCBBF3013307, FEBRA2026984,
 SPLEN2010912, TBAES2001171, TESTI2040018, TESTI4019566,
 TESTI4022716, TESTI4026510, TESTI4036909, THYMU3000133,
 35 TRACH2023299, TRACH3036193, UTERU1000024, UTERU3002993

The following eleven clones are also predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein.

BRACE3003053, BRCAN2002473, BRTHA2017364, NT2RI2008952,
 5 NT2RI3000174, TESTI2026647, TESTI2035981, TESTI4000155,
 TESTI4006473, TESTI4010382, TESTI4025547

The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 29 clones.

10 BRACE2014306, BRACE3008720, BRAWH3000491, BRCAN2009432,
 BRHIP2000920, BRTHA3013884, CTONG2013178, HCHON2004531,
 HLUNG1000017, HLUNG2013851, HSYRA2005496, NT2NE2006909,
 NT2RI3006340, OCBBF2007068, OCBBF2031167, PUAEN2009795,
 TBAES2001229, TBAES2004055, TESTI2051867, TESTI4000014,
 15 TESTI4000349, TESTI4009608, TESTI4010851, TESTI4034632,
 TRACH3007479, TRACH3036193, UTERU2017762, UTERU2019940,
 UTERU2033375

The following 17 clones are also predicted to belong to the category of protein synthesis and/or transport-related protein.

20 BLADE2000579, BRACE3003053, BRCAN2003070, BRTHA2018011,
 BRTHA3000296, CTONG2016942, MESAN2005303, NT2RI3002557,
 NT2RP7008435, PERIC2007068, PLACE7000502, PROST2000452,
 TESTI4001984, TESTI4017714, THYMU2004284, TRACH3000420,
 TRACH3007866

25 The clones predicted to belong to the category of cellular defense-related protein are the following four clones.

BRTHA2015878, CTONG3000084, NT2RI3002842, PEBLM2004666

The following three clones are also predicted to belong to the category of cellular defense-related protein.

30 BRCAN2002473, NT2RI3007167, TRACH3002561

The clone predicted to belong to the category of development and/or differentiation-related protein is the following one clone.

TESTI4014924

35 The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 67 clones.

BRACE2006319, BRACE2047011, BRACE3004150, BRACE3013576,
 BRACE3024073, BRAMY2030109, BRAWH3005912, BRCAN2002562,
 BRCOC2003213, BRHIP2021615, BRHIP3008183, BRHIP3025161,
 BRSTN2004987, BRTHA2018707, BRTHA3016917, CORDB1000140,
 5 CTONG1000467, CTONG3000084, CTONG3003972, CTONG3008831,
 CTONG3009028, FCBBF3013307, FEBRA2026984, HEART2001756,
 HLUNG2013851, IMR322000127, IMR322000917, KIDNE1000064,
 NT2NE2006531, NT2RI3003382, NT2RI3007158, NT2RP7000466,
 NT2RP7004123, OCBBF2036743, OCBBF3009279, PLACE6019385,
 10 SPLEN2006122, SPLEN2010912, TESOP2009121, TESTI1000390,
 TESTI2014716, TESTI2026505, TESTI2040018, TESTI2044796,
 TESTI2050987, TESTI4007810, TESTI4009374, TESTI4011745,
 TESTI4012679, TESTI4017001, TESTI4019140, TESTI4019566,
 TESTI4022716, TESTI4026510, TESTI4034432, TESTI4034912,
 15 TESTI4036909, THYMU2035319, THYMU2035735, THYMU3000133,
 TLIVE2002336, TRACH2023299, TRACH2025749, TRACH3004840,
 TRACH3036193, UTERU2026025, UTERU3009490

The following 112 clones are also predicted to belong to
 the category of DNA-binding and/or RNA-binding protein.

20 BLADE2006830, BRACE2003609, BRACE3001058, BRACE3001113,
 BRACE3003026, BRACE3003053, BRACE3010076, BRAMY2035070,
 BRAMY2035449, BRAMY2039341, BRAMY2045471, BRAWH1000369,
 BRAWH3007441, BRHIP2017553, BRSTN2013354, BRTHA2002133,
 BRTHA2002702, BRTHA2017364, BRTHA2017972, CERVX2002013,
 25 CTONG1000113, CTONG2003348, CTONG2015596, CTONG2020374,
 CTONG2020378, CTONG2020411, CTONG2024031, CTONG2028758,
 CTONG3001501, CTONG3004726, DFNES2011192, FCBBF1000509,
 FCBBF3027854, FEBRA2014122, FEBRA2027609, HCASM2003018,
 HCASM2003099, HCASM2009424, HCHON2000508, HCHON2000743,
 30 HCHON2004858, HSYRA2005628, IMR322013731, MESAN2014412,
 MESAN2015501, NT2RI2008952, NT2RI2018448, NT2RI2027157,
 NT2RI3000174, NT2RI3001132, NT2RI3002557, NT2RI3007167,
 NT2RI3007443, OCBBF2006987, OCBBF2008144, OCBBF2009583,
 OCBBF2011669, OCBBF2019684, OCBBF2020048, OCBBF2024284,
 35 OCBBF2032274, OCBBF2034637, OCBBF3000167, OCBBF3003761,
 PERIC2007068, SPLEN2016135, SPLEN2016781, SPLEN2036702,

STOMA2003158, SYNOV2021953, SYNOV4002744, TESOP2001796,
 TESOP2005199, TESOP2006398, TESTI2008901, TESTI2026647,
 TESTI2034251, TESTI2035981, TESTI2037830, TESTI4000155,
 TESTI4000183, TESTI4000214, TESTI4006473, TESTI4008058,
 5 TESTI4008302, TESTI4010382, TESTI4013365, TESTI4014801,
 TESTI4015442, TESTI4017714, TESTI4025494, TESTI4025547,
 TESTI4026207, TESTI4028938, TESTI4028958, TESTI4029348,
 TESTI4031745, TESTI4032090, THYMU2006001, THYMU2028739,
 THYMU2031139, THYMU3001428, TKIDN2012771, TLIVE2007607,
 10 TRACH2007483, TRACH3000134, TRACH3003832, TRACH3007866,
 UTERU3001053, UTERU3014791, UTERU3017176, TESTI4038779

The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 28 clones.

BRACE3008720, BRACE3009708, BRAMY2047746, BRAMY3004919,
 15 BRAWH2014662, BRAWH2016702, BRCAN2009432, BRCAN2024451,
 BRSTN2013741, BRTHA3008778, BRTHA3009090, CTONG2004062,
 CTONG2028124, HCHON2004007, OCBBF2037340, SPLEN2030335,
 TESTI4000288, TESTI4001148, TESTI4002552, TESTI4008429,
 TESTI4018835, TESTI4021478, TESTI4029836, THYMU2036459,
 20 THYMU3001379, TRACH2001549, UTERU3000828, UTERU3001240

The following eight clones are also predicted to belong to the category of ATP binding and/or GTP-binding protein.

BRCAN2014229, BRHIP2008389, CTONG3004550, FEBRA2001990,
 IMR322013396, IMR322013731, MESAN2001770, TESTI4000319

25 Although the 208 clones described below have hit data in Pfam, it remains unclear as to which of the above-described categories each of these clones belong. However, if data for proteins having a similar domain or motif are accumulated and their functions clarified in more detail, in the future these
 30 clones can be classified into any of the above-described categories. The Clone Name and Functional Domain Name are indicated as "Clone Name//Functional Domain Name". When a clone had hit data in multiple functional domains, all data were represented, with each marked with a double slash (/).

In addition, even when a clone had multiple hit data in an identical functional domain, these data are fully represented without abridgment.

- 3NB692002685 //R3H domain
- 5 3NB692008729 //Hr1 repeat motif
- ASTRO2003960 //F-box domain.
- BNGH42003570 //EB module// Furin-like cysteine rich region//
Thrombospondin type 1 domain
- BRACE2010489 //LysM domain
- 10 BRACE2015314 //Bacterial mutT protein
- BRACE2016981 //Fanconi anaemia group C protein// Bacterial
flagellin N-terminus
- BRACE2027258 //Ank repeat// Ank repeat// Ank repeat// Ank
repeat// Ank repeat
- 15 BRACE2030341 //Kinase associated domain 1
- BRACE2035441 //Spectrin repeat// Spectrin repeat// Spectrin
repeat
- BRACE2038329 //TS-N domain// UBA domain
- BRACE2042550 //Thrombospondin type 1 domain// Trypsin Inhibitor
- 20 like cysteine rich domain// von Willebrand factor type C
domain// Thrombospondin type 1 domain
- BRACE2044286 //CRAL/TRIO domain.// Spectrin repeat
- BRACE3000071 //Ank repeat// Ank repeat// Ank repeat
- BRACE3000973 //Leucine Rich Repeat
- 25 BRACE3001002 //Lipoprotein
- BRACE3003192 //EGF-like domain// EGF-like domain// EGF-like
domain// EGF-like domain// Metallothionein// Keratin, high
sulfur B2 protein// EGF-like domain// EGF-like domain// EGF-like
domain// EGF-like domain// TB domain// EGF-like domain// EGF-
- 30 like domain// EGF-like domain// TB domain// EGF-like domain//
EGF-like domain
- BRACE3004772 //SAM domain (Sterile alpha motif)
- BRACE3004880 //GLTT repeat (12 copies)// GLTT repeat (12
copies)// GLTT repeat (12 copies)// Keratin, high sulfur B2
- 35 protein
- BRACE3008137 //PDZ domain (Also known as DHR or GLGF).// PDZ

domain (Also known as DHR or GLGF). // PDZ domain (Also known as
 DHR or GLGF). // PDZ domain (Also known as DHR or GLGF).
 BRACE3008384 //Rhomboid family
 BRACE3009090 //Beige/BEACH domain
 5 BRACE3010397 //SCP-like extracellular protein
 BRACE3015521 //EF hand
 BRACE3016884 //Keratin, high sulfur B2 protein// Flagellar L-
 ring protein
 BRACE3019084 //SAM domain (Sterile alpha motif)
 10 BRAMY2004771 //Leucine Rich Repeat// Leucine rich repeat C-
 terminal domain// Leucine rich repeat N-terminal domain
 BRAMY2019300 //Leucine Rich Repeat// Leucine rich repeat C-
 terminal domain// Leucine rich repeat N-terminal domain
 BRAMY2021498 //Thrombospondin type 1 domain// DnaJ central
 15 domain (4 repeats)// Thrombospondin type 1 domain//
 Thrombospondin type 1 domain// Thrombospondin type 1 domain//
 Thrombospondin type 1 domain
 BRAMY2031317 //PDZ domain (Also known as DHR or GLGF).
 BRAMY2039872 //Interferon alpha/beta domain
 20 BRAMY2046989 //TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// TPR Domain// TPR Domain
 BRAMY3004224 //Leucine rich repeat N-terminal domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat
 25 C-terminal domain
 BRAMY3005932 //Ank repeat
 BRAWH1000127 //Plexin repeat// Thrombospondin type 1 domain
 BRAWH2001395 //Myelin basic protein
 BRAWH2014954 //PDZ domain (Also known as DHR or GLGF). // PDZ
 30 domain (Also known as DHR or GLGF).
 BRAWH3000078 //Adaptin N terminal region// Activin types I and
 II receptor domain
 BRAWH3001891 //YCF9
 BRAWH3002574 //Calpain large subunit, domain III// EF hand
 35 BRAWH3002600 //Cadherin domain// Cadherin domain// Cadherin
 domain

BRAWH3008341 //Pentaxin family
 BRCAN2002948 //Adaptin N terminal region
 BRCAN2009203 //SAM domain (Sterile alpha motif)
 BRCAN2015464 //Gag P30 core shell protein
 5 BRCAN2017717 //Squash family of serine protease inhibitors
 BRCOC2001505 //Myelin basic protein
 BRCOC2016525 //Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat
 BRHIP2003786 //Ank repeat// Ank repeat// Ank repeat// BTB/POZ
 10 domain
 BRHIP2005236 //Galactose binding lectin domain// Latrophilin
 Cytoplasmic C-terminal region
 BRHIP2007616 //Sema domain
 BRHIP2009414 //Uncharacterized protein family
 15 BRHIP3000339 //Myelin basic protein
 BRHIP3008313 //Ank repeat
 BRSTN2001067 //Rifin/stevor family
 BRTHA2000855 //Extracellular link domain
 BRTHA2005579 //von Willebrand factor type C domain// von
 20 Willebrand factor type C domain// von Willebrand factor type C
 domain// von Willebrand factor type C domain// von Willebrand
 factor type C domain// von Willebrand factor type C domain// von
 Willebrand factor type C domain// von Willebrand factor type C
 domain// von Willebrand factor type C domain// von Willebrand
 25 factor type C domain// von Willebrand factor type C domain// von
 Willebrand factor type C domain
 BRTHA2007122 //Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// SAM domain (Sterile alpha motif)
 BRTHA2008527 //Leucine Rich Repeat// Leucine Rich Repeat//
 30 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 BRTHA2009311 //Vertebrate galactoside-binding lectins
 BRTHA2010884 //Thrombospondin type 1 domain// CUB domain
 BRTHA2013262 //Keratin, high sulfur B2 protein
 BRTHA2014792 //SET domain
 35 BRTHA2015406 //UBA domain
 BRTHA2016496 //Peptidase C13 family

BRTHA2018591 //GTPase of unknown function
 BRTHA2018624 //Galactose binding lectin domain// Activin types I
 and II receptor domain// Galactose binding lectin domain
 BRTHA2019048 //Domain of unknown function DUF71
 5 BRTHA3003074 //Fanconi anaemia group C protein
 BRTHA3008310 //Homeobox domain
 CTONG1000341 //EGF-like domain// EGF-like domain//
 Metallothionein// EGF-like domain// EB module// EGF-like
 domain// EGF-like domain// EGF-like domain
 10 CTONG2001877 //MutT-like domain
 CTONG2008233 //DnaJ domain
 CTONG2017500 //F-box domain.
 CTONG2020026 //Herpesvirus VP23 like capsid protein
 CTONG2028687 //TPR Domain// TPR Domain
 15 CTONG3000686 //TPR Domain// TPR Domain// TPR Domain// TPR Domain
 CTONG3004072 //Beta type Zein// Keratin, high sulfur B2 protein
 CTONG3006067 //DnaJ central domain (4 repeats)
 CTONG3006186 //PDZ domain (Also known as DHR or GLGF)//
 Apolipoprotein A1/A4/E family// WW domain
 20 CTONG3009385 //TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// TPR Domain
 DFNES2000146 //Plexin repeat// Thrombospondin type 1 domain
 DFNES2005266 //Thrombospondin type 1 domain
 25 FCBBF3009888 //Keratin, high sulfur B2 protein// u-PAR/Ly-6
 domain
 FCBBF3012170 //Thrombospondin type 1 domain
 FEBRA2000253 //Flagellar L-ring protein
 FEBRA2007801 //IBR domain
 30 FEBRA2021571 //von Willebrand factor type D domain
 FEBRA2024150 //DENN (AEX-3) domain
 HCHON2004776 //Protein of unknown function DUF93
 HEART1000139 //Troponin
 HEART2006909 //CBS domain// CBS domain
 35 HEART2010495 //Tau and MAP proteins, tubulin-binding
 HLUNG2000014 //Lectin C-type domain

HLUNG2002958 //EF hand
 HLUNG2011298 //Oxidoreductase FAD/NAD-binding domain
 IMR322006495 //Tropomyosins
 KIDNE2000846 //Sodium:neurotransmitter symporter family
 5 KIDNE2001361 //Domain of unknown function DUF19
 KIDNE2011635 //Sodium:solute symporter family
 KIDNE2012945 //CUB domain// Pentaxin family
 NESOP2001656 //Polyomavirus coat protein
 NT2RI2008724 //GGL domain
 10 NT2RI2025909 //Mitochondrial carrier proteins// Mitochondrial
 carrier proteins// Mitochondrial carrier proteins
 NT2RI2025957 //PDZ domain (Also known as DHR or GLGF).
 NT2RI3007543 //DnaJ domain
 NT2RP7000359 //FERM domain (Band 4.1 family)// Insulin-like
 15 growth factor binding proteins// PDZ domain (Also known as DHR
 or GLGF).
 NT2RP7004027 //CUB domain// Sushi domain (SCR repeat)
 NT2RP7011570 //Gag P30 core shell protein
 NT2RP8000296 //BTB/POZ domain// Kelch motif// Kelch motif//
 20 Kelch motif// Kelch motif// Kelch motif// Kelch motif
 NTONG2005277 //Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 NTONG2006354 //Ank repeat
 NTONG2007517 //BTB/POZ domain
 25 OCBBF2006764 //Sushi domain (SCR repeat)// CUB domain// Sushi
 domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)
 OCBBF2010416 //Major intrinsic protein
 OCBBF2020838 //Fork head domain
 OCBBF2021323 //Regulatory subunit of type II PKA R-subunit
 30 OCBBF2033869 //CUB domain
 PERIC2001228 //Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 PERIC2003720 //Ezrin/radixin/moesin family
 35 PLACE6020031 //Ank repeat// Ank repeat
 PLACE7000514 //Filamin/ABP280 repeat.

PROST2018090 //Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Chitin binding Peritrophin-A domain// HYR domain// Sushi domain (SCR repeat)
 RECTM2000433 //Jacalin-like lectin domain
 5 SKMUS2006394 //Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 SMINT1000192 //Small hydrophilic plant seed proteins
 SPLEN2002147 //Phosphatidylinositol transfer protein
 SPLEN2002467 //DB module// F-box domain.// Leucine Rich Repeat
 10 SPLEN2031780 //Domain of unknown function DUF139// Domain of unknown function DUF139
 SPLEN2034081 //Insulin-like growth factor binding proteins
 SPLEN2036821 //Mitochondrial carrier proteins
 SYNOV2005448 //Apidaecin
 15 SYNOV2005817 //Domain of unknown function DUF19// Tissue factor
 SYNOV2006430 //Nitrogen regulatory protein P-II
 SYNOV2014400 //EGF-like domain// Granulins// Granulins// EGF-like domain
 SYNOV4007553 //Leucine Rich Repeat// Leucine Rich Repeat//
 20 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat
 C-terminal domain// TIR domain
 25 SYNOV4008440 //Adaptin N terminal region
 TESOP2001953 //Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 TESTI2000443 //Leucine Rich Repeat// Leucine Rich Repeat//
 30 Leucine Rich Repeat
 TESTI2004700 //Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 TESTI2027019 //Leucine Rich Repeat
 TESTI4000462 //Keratin, high sulfur B2 protein
 35 TESTI4000970 //Ezrin/radixin/moesin family
 TESTI4002491 //NSF attachment protein

TESTI4006546 //Tudor domain// Tudor domain// Tudor domain
 TESTI4007064 //DENN (AEX-3) domain// PPR repeat// LIM domain
 containing proteins
 TESTI4011484 //SAM domain (Sterile alpha motif)
 5 TESTI4012406 //Kringle domain
 TESTI4015471 //Tropomyosins
 TESTI4016110 //DnaJ domain
 TESTI4017137 //Keratin, high sulfur B2 protein
 TESTI4017575 //MSP (Major sperm protein) domain
 10 TESTI4018152 //FERM domain (Band 4.1 family)
 TESTI4018555 //Granulins
 TESTI4020092 //Laminin G domain
 TESTI4023555 //Lectin C-type domain
 TESTI4025920 //Adaptin N terminal region
 15 TESTI4026192 //Domain of unknown function
 TESTI4027557 //Vertebrate galactoside-binding lectins//
 Vertebrate galactoside-binding lectins
 TESTI4028429 //WAP-type (Whey Acidic Protein) 'four-disulfide
 core'
 20 TESTI4028612 //Major intrinsic protein
 TESTI4028983 //Serum amyloid A protein
 TESTI4030505 //Metallothionein family 5
 TESTI4038492 //Serum amyloid A protein
 TESTI4039659 //DnaJ domain
 25 TESTI4041053 //Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// Armadillo/beta-catenin-like repeats// Armadillo/beta-
 catenin-like repeats// Armadillo/beta-catenin-like repeats//
 Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-
 like repeats// Armadillo/beta-catenin-like repeats
 30 TESTI4044084 //Domain of unknown function
 TESTI4046487 //Hantavirus nucleocapsid protein
 TESTI4046819 //Metallothionein// PTS HPr component
 phosphorylation sites
 THYMU2004693 //CX module
 35 THYMU2011736 //EGF-like domain// EGF-like domain// EB module//
 EGF-like domain// TB domain// EGF-like domain// EGF-like domain

THYMU2016204 //Metallothionein
 THYMU2027734 //Parvovirus coat protein VP2
 THYMU2038369 //Regulatory subunit of type II PKA R-subunit
 THYMU2038797 //Lectin C-type domain
 5 THYMU3000028 //Zona pellucida-like domain
 THYMU3003212 //Cytidine and deoxycytidylate deaminase zinc-binding region
 THYMU3003763 //Leucine rich repeat N-terminal domain// Polyomavirus coat protein
 10 THYMU3007137 //PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).
 THYMU3008171 //TPR Domain
 TLIVE2002338 //Transforming growth factor beta like domain
 TLIVE2002690 //von Willebrand factor type D domain
 15 TLIVE2003225 //CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)
 TLIVE2008229 //TPR Domain// TPR Domain
 TRACH2001443 //TIR domain
 TRACH3001427 //UBX domain
 20 TRACH3003379 //Protein phosphatase 2A regulatory B subunit
 TRACH3008713 //NSF attachment protein
 TRACH3035235 //S-100/ICaBP type calcium binding domain
 TUTER2000425 //KRAB box
 UTERU1000031 //ENTH domain// VHS domain
 25 UTERU2006115 //Adaptin N terminal region
 UTERU2006568 //IBR domain
 UTERU2019706 //TCP-1/cpn60 chaperonin family// TCP-1/cpn60 chaperonin family
 UTERU2035328 //WW domain// WW domain// WW domain// FF domain//
 30 FF domain// FF domain
 UTERU2035331 //Fibrillar collagen C-terminal domain
 UTERU2035452 //EGF-like domain// Metallothionein// EGF-like domain
 UTERU3001652 //Wiskott Aldrich syndrome homology region 2
 35 UTERU3001766 //Apidaecin
 UTERU3001988 //TPR Domain

- UTERU3002667 //Polyomavirus coat protein
 UTERU3003178 //TPR Domain// TPR Domain// TPR Domain// TPR
 Domain// PPR repeat
 UTERU3005585 //PDZ domain (Also known as DHR or GLGF).
 5 UTERU3007640 //NSF attachment protein
 UTERU3008660 //TPR Domain// TPR Domain
 UTERU3009871 //Ank repeat// Ank repeat// Ank repeat// Ank
 repeat// TPR Domain// Ank repeat// Ank repeat
 UTERU3009979 //EGF-like domain// EGF-like domain// EGF-like
 10 domain// Trypsin Inhibitor like cysteine rich domain// EGF-like
 domain// Laminin G domain// Thrombospondin N-terminal -like
 domains// Laminin G domain
 UTERU3015500 //Leucine rich repeat N-terminal domain// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 15 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat

Likewise, although the 45 clones described below have hit
 data in Pfam (see Example 5), it remains unclear as to which of
 20 the above-described categories each of the clones belong.
 However, if data for proteins comprising a similar domain or
 motif are accumulated and their functions are clarified in more
 detail, in the future these clones can be classified into any of
 the categories described above.

- 25 3NB692004724// KRAB box// Integrase core domain
 ADRGL2000042// Nucleosome assembly protein (NAP)
 BRACE2037299// Integrase core domain
 BRALZ2017844// Homeobox domain
 BRAWH2006207// KRAB box
 30 BRCAN2002854// SAP domain
 BRHIP2006617// TPR Domain// TPR Domain
 BRHIP2012360// XPG N-terminal domain// XPG I-region
 BRHIP3008314// Sir2 family
 BRTHA2016318// KE2 family protein
 35 CTONG2019822// Hepatitis C virus core protein
 FCBBF3010361// Fork head domain

FEBRA2006519// Thrombospondin type 1 domain// Thrombospondin
 type 1 domain
 FEBRA2028256// EGF-like domain// EGF-like domain// EGF-like
 domain// EGF-like domain// EGF-like domain// TB domain// EGF-
 5 like domain// EGF-like domain// EGF-like domain// EGF-like
 domain// EB module// Squash family of serine protease
 inhibitors// EGF-like domain// EGF-like domain
 FEBRA2028516// GRIP domain
 HCASM2008536// XRCC1 N terminal domain
 10 IMR322007078// UBA domain
 IMR322008651// Helix-hairpin-helix motif.
 LIVER2000247// Sodium
 OCBBF2003327// Thrombospondin type 1 domain// Thrombospondin
 type 1 domain// Thrombospondin type 1 domain
 15 PROST2009320// LIM domain containing proteins// LIM domain
 containing proteins
 PUAEN2006335// Formin Homology 2 Domain
 SKMUS2003194// SAP domain
 SPLEN2039379// Transthyretin precursor (formerly prealbumin)
 20 SYNOV1000256// Leucine Rich Repeat// BAH domain// Leucine Rich
 Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 SYNOV2006620// Nuclear transition protein 2
 SYNOV4003981// Somatomedin B domain// WAP-type (Whey Acidic
 Protein) 'four-disulfide core'// Hemopexin// Hemopexin
 25 SYNOV4005889// Apolipoprotein A1/A4/E family
 TESOP2006865// KRAB box
 TESTI1000266// Integrase core domain
 TESTI2050780// Kazal-type serine protease inhibitor domain
 TESTI4000137// Domain of unknown function
 30 TESTI4024387// GDP dissociation inhibitor
 TESTI4029528// RanBP1 domain.
 TESTI4038721// Squash family of serine protease inhibitors
 TESTI4046240// Sir2 family
 THYMU2035078// Domain of unknown function DUF27
 35 THYMU3000269// FAD binding domain
 THYMU3000360// Integrase core domain

TRACH1000212// TSC-22/dip/bun family
 TRACH2000862// Guanylate-binding protein
 TRACH2019672// CRAL/TRIO domain.
 TRACH2024559// IQ calmodulin-binding motif// IQ calmodulin-
 5 binding motif
 UTERU2032279// Serpins (serine protease inhibitors)
 UTERU2033577// KRAB box

In addition, when data for proteins are accumulated and novel domains and motifs are found, in the future the remaining
 10 clones, which had no hit data in the search with Pfam, can be classified into any of the above-described categories if a new functional domain or motif is identified by re-analyzing the deduced amino acid sequences of the clones using a homology search against an updated database.

EXAMPLE 8

Expression frequency analysis in silico

The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were
 20 selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 1,402,069 clones, and thus the population of the database is large enough for the analysis.

25 Then, clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search; the number of clones belonging to each cluster was determined and normalized for
 30 every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

35 Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a

tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 2 to 24 shown below represents a relative expression frequency; the higher the value, the higher the expression level. The genes which are included a part of the Tables indicate not so big difference between compared libraries, but when compared with other libraries from another tissue or cell based on Example 9, they indicate significant difference. Thus, the genes are specific in each tissue or cell, and can be considered to be useful as diagnosing markers for the disease as well as useful for analyzing molecular mechanisms.

Osteoporosis-related genes

Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from

the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following 15 and 2 clones (Table 2).

BRACE3013780, BRAMY2047420, BRSTN2016470, CTONG3008894, D3OST2002182, D3OST2002648, D3OST3000169, PEBLM2005183, PUAEN2009655, TESTI4000014, TESTI4010851, TRACH2023299, TRACH2025535, TRACH3001427, UTERU2006137
HCHON2000508, TESTI2015626

These genes are involved in osteoporosis.

Genes involved in neural cell differentiation

Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following 174 and 30 clones (Table 3).

BNGH42007788, BRACE1000186, BRACE2006319, BRACE2014306, BRACE2015058, BRACE2044286, BRACE3010428, BRAMY2044078, BRAWH2014645, BRAWH2014662, BRAWH3002574, BRAWH3003992, BRAWH3005981, BRAWH3007592, BRCAN2009432, BRCAN2016619, BRCAN2028355, BRHIP2001074, BRHIP2007741, BRHIP2014228, BRHIP2024146, BRHIP3007586, BRHIP3018797, BRTHA2003461, BRTHA3000633, BRTHA3003490, COLON2001721, CTONG1000087, CTONG2008233, CTONG2020638, CTONG2028124, CTONG3003905, CTONG3008894, CTONG3009028, CTONG3009239, DFNES2011499,

FCBBF3001977, FEBRA1000030, FEBRA2006396, FEBRA2007801,
 HCHON2000028, HCHON2000244, HCHON2001084, HCHON2001217,
 HCHON2001548, HCHON2006250, HEART1000074, HHDP1000118,
 HSYRA2009075, IMR322000127, IMR322001380, KIDNE2000665,
 5 KIDNE2002252, MESAN2006563, MESAN2012054, MESAN2015515,
 NT2NE2003252, NT2NE2005890, NT2NE2006531, NT2NE2006909,
 NT2NE2008060, NT2RI2003993, NT2RI2004618, NT2RI2005166,
 NT2RI2006686, NT2RI2008724, NT2RI2009855, NT2RI2011422,
 NT2RI2011683, NT2RI2012659, NT2RI2012990, NT2RI2013357,
 10 NT2RI2014247, NT2RI2014551, NT2RI2014733, NT2RI2016128,
 NT2RI2018311, NT2RI2018883, NT2RI2019751, NT2RI2023303,
 NT2RI2025909, NT2RI2025957, NT2RI2027081, NT2RI2027396,
 NT2RI3000622, NT2RI3001263, NT2RI3001515, NT2RI3002303,
 NT2RI3002842, NT2RI3002892, NT2RI3003031, NT2RI3003095,
 15 NT2RI3003162, NT2RI3003382, NT2RI3003409, NT2RI3004381,
 NT2RI3004510, NT2RI3005202, NT2RI3005403, NT2RI3005724,
 NT2RI3006132, NT2RI3006171, NT2RI3006284, NT2RI3006340,
 NT2RI3006376, NT2RI3006673, NT2RI3006796, NT2RI3007065,
 NT2RI3007158, NT2RI3007291, NT2RI3007543, NT2RI3007757,
 20 NT2RI3007978, NT2RI3008055, NT2RI3008162, NT2RI3008652,
 NT2RI3008697, NT2RI3008974, NT2RI3009158, NT2RP7000359,
 NT2RP7000466, NT2RP7004027, NT2RP7004123, NT2RP7005118,
 NT2RP7005529, NT2RP7005846, NT2RP7009030, NT2RP7009147,
 NT2RP7009867, NT2RP7010128, NT2RP7010599, NT2RP7011570,
 25 NT2RP7013795, NT2RP7014005, NT2RP7015512, NT2RP7017365,
 NT2RP7017474, NT2RP7017546, NT2RP8000137, NT2RP8000296,
 NT2RP8000483, NTONG2005969, OCBBF2007028, OCBBF2037068,
 PLACE7000514, PUAEN2007044, SPLEN2002467, SPLEN2006122,
 SPLEN2028914, SPLEN2031547, SYNOV4002346, SYNOV4007671,
 30 SYNOV4008440, TESOP2002273, TESTI2003573, TESTI4000014,
 TESTI4009286, TESTI4010851, TESTI4012702, TESTI4029671,
 TESTI4037156, THYMU3000133, TRACH1000205, TRACH2005811,
 TRACH2007834, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004721, TRACH3008093, TRACH3008535, TRACH3008713,
 35 UTERU2002410, UTERU2023175

ADRGL2000042, BRACE2003609, BRACE3003026, BRHIP3000017,
 CTONG2020411, FCBBF1000509, FCBBF3027854, FEBRA2028516,
 HCHON2000508, IMR322001879, NT2RI2005772, NT2RI2008952,
 NT2RI2009583, NT2RI2018448, NT2RI2027157, NT2RI3000174,
 5 NT2RI3001132, NT2RI3002557, NT2RI3005928, NT2RI3007167,
 NT2RI3007443, NT2RP7008435, NT2RP8000521, OCBBF2006987,
 PERIC2007068, TESTI2015626, TESTI4015442, TLIVE2002046,
 TRACH3000134, TUTER2000057

These genes are neurological disease-related genes.

10

Genes involved in Alzheimer's disease

Alzheimer's disease is a cranial neurological disease that
 is characterized by memory loss. As the disease advances,
 patients can no longer support themselves and require nursing.
 15 Alzheimer's disease eventually leads to atrophication of the
 brain itself. Environmental factors such as stress, and
 vascular factors such as hypertension and cholesterolemia, are
 assumed, but not confirmed, to contribute to the onset of
 Alzheimer's disease. Genes whose expression levels differ
 20 between normal brain tissues and tissues affected with
 Alzheimer's disease are expected to be involved in Alzheimer's
 disease. Such genes can be used to elucidate the disease's
 onset mechanism and in genetic diagnosis. cDNA libraries
 derived from the cerebral cortex of Alzheimer patients (BRALZ
 25 and BRASW), and a library derived from whole tissues of a normal
 brain (BRAWH) were analyzed and compared (Table 4). The results
 showed that genes whose expression levels differed between the
 two are the following 250 and 41 clones listed below.

ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 30 BRACE1000533, BRACE2005457, BRACE2010489, BRACE2014657,
 BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,
 BRACE3003192, BRACE3005499, BRACE3007480, BRACE3009237,
 BRACE3009724, BRACE3009747, BRACE3010428, BRACE3011271,
 BRACE3011421, BRACE3012364, BRACE3022769, BRACE3026735,
 35 BRACE3031838, BRALZ2011796, BRALZ2012183, BRALZ2012848,
 BRALZ2014484, BRALZ2016085, BRALZ2016498, BRALZ2017359,

BRAMY2003008, BRAMY2005052, BRAMY2019300, BRAMY2019963,
 BRAMY2036567, BRAMY2037823, BRAMY2040592, BRAMY3002803,
 BRAMY3004224, BRAMY3005091, BRASW1000053, BRASW1000125,
 BRAWH1000127, BRAWH2001395, BRAWH2001671, BRAWH2001940,
 5 BRAWH2001973, BRAWH2002560, BRAWH2002761, BRAWH2005315,
 BRAWH2007658, BRAWH2010000, BRAWH2010084, BRAWH2010536,
 BRAWH2012162, BRAWH2012326, BRAWH2013294, BRAWH2013871,
 BRAWH2014414, BRAWH2014645, BRAWH2014662, BRAWH2014876,
 BRAWH2014954, BRAWH2016221, BRAWH2016439, BRAWH2016702,
 10 BRAWH2016724, BRAWH3000078, BRAWH3000100, BRAWH3000314,
 BRAWH3000491, BRAWH3001326, BRAWH3001475, BRAWH3001891,
 BRAWH3002574, BRAWH3002600, BRAWH3002819, BRAWH3002821,
 BRAWH3003522, BRAWH3003555, BRAWH3003727, BRAWH3003801,
 BRAWH3003992, BRAWH3004453, BRAWH3004666, BRAWH3005132,
 15 BRAWH3005422, BRAWH3005912, BRAWH3005981, BRAWH3006548,
 BRAWH3006792, BRAWH3007221, BRAWH3007506, BRAWH3007592,
 BRAWH3007726, BRAWH3007783, BRAWH3008341, BRAWH3008697,
 BRAWH3008931, BRAWH3009297, BRCOC2003213, BRCOC2014033,
 BRCOC2020142, BRHIP2000920, BRHIP2005719, BRHIP2007741,
 20 BRHIP2014228, BRHIP2024146, BRHIP2026288, BRHIP3000339,
 BRHIP3006683, BRHIP3007586, BRHIP3008405, BRHIP3018797,
 BRSSN2000684, BRSSN2011738, BRSSN2014299, BRSTN2008052,
 BRSTN2015015, BRSTN2016470, BRTHA1000311, BRTHA2008335,
 BRTHA3002427, BRTHA3003490, BRTHA3008520, BRTHA3017848,
 25 COLON2001721, CTONG2017500, CTONG2028124, CTONG3000657,
 CTONG3001123, CTONG3009328, FCBBF2001183, FCBBF3001977,
 FEBRA2007544, FEBRA2007801, FEBRA2020886, FEBRA2028618,
 HCASM2007047, HCHON2000244, HCHON2000626, HCHON2001217,
 HCHON2002676, HCHON2006250, HEART1000074, HHDPC1000118,
 30 HLUNG2002465, IMR322000127, IMR322001380, IMR322002035,
 KIDNE2006580, MESAN2006563, MESAN2012054, MESTC1000042,
 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
 NT2RI2014733, NT2RI3002892, NT2RI3006284, NT2RI3006673,
 NT2RI3007543, NT2RI3008055, NT2RP7005529, NT2RP7009147,
 35 NT2RP7014005, NT2RP7017474, NTONG2005969, OCBBF2001794,
 OCBBF2006005, OCBBF2006764, OCBBF2007028, OCBBF2007114,

OCBBF2010140, OCBBF2021286, OCBBF2023162, OCBBF2024850,
 OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,
 PUAEN2006701, PUAEN2007044, PUAEN2009655, SMINT2001818,
 5 SPLEN2028914, SPLEN2031424, SPLEN2031547, SPLEN2034781,
 SPLEN2036932, SYNOV2014400, SYNOV4002346, SYNOV4002883,
 SYNOV4007430, SYNOV4007671, SYNOV4008440, TESOP2002273,
 TESOP2002451, TESTI4000014, TESTI4000209, TESTI4001100,
 TESTI4006137, TESTI4008797, TESTI4009286, TESTI4010851,
 10 TESTI4013817, TESTI4014694, TESTI4021478, TESTI4022936,
 TESTI4024420, TESTI4027821, THYMU2001090, THYMU2033308,
 THYMU2035735, THYMU2039315, THYMU3001234, THYMU3008171,
 TKIDN2009641, TKIDN2009889, TKIDN2015788, TRACH1000205,
 TRACH2001549, TRACH2005811, TRACH2006049, TRACH2007834,
 15 TRACH2008300, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004068, TRACH3004721, TRACH3005294, TRACH3007479,
 TRACH3008093, TRACH3009455, UTERU2005621, UTERU2006115,
 UTERU2019706, UTERU2023039, UTERU2026203, UTERU3005230,
 UTERU3007640, UTERU3009871
 20 ADRGL2000042, BLADE2006830, BRACE2003609, BRALZ2017844,
 BRAMY3004800, BRAWH1000369, BRAWH2006207, BRAWH2006395,
 BRAWH2008993, BRAWH2009393, BRAWH2010552, BRAWH3007441,
 BRAWH3009017, BRHIP2005271, BRHIP3000017, BRHIP3026052,
 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 25 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000743, IMR322001879, NT2RI2009583,
 OCBBF2008144, PERIC2007068, PUAEN2006335, SPLEN2039379,
 TESTI4001984, TESTI4008058, TESTI4025268, TESTI4032090,
 THYMU3000360, TLIVE2002046, TRACH3000134, UTERU2021820,
 30 UTERU2028734

These genes are involved in Alzheimer's disease.

Genes involved in Parkinson's disease

Parkinson's disease is a cranial neurological disease
 35 characterized by impaired production of the neurotransmitter
 dopamine in the substantia nigra in the brain. This results in

dyskinesia, such as hand tremors, and impaired body movement due to muscular rigidity. Normally, the number of brain neurons gradually decreases with age. However, compared to healthy people, patients with Parkinson's disease experience a rapid and marked decrease in the number of neurons in their substantia nigra. Genes whose expression levels differ between tissues of the whole brain and the nigra are expected to be involved in Parkinson's disease. These genes exhibit nigra-specific alterations in their expression levels, and can be used to elucidate the disease onset mechanism and in gene diagnosis. cDNA libraries derived from the substantia nigra (BRSSN) and a library derived from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 5). Genes whose expression levels differed between the two were the 250 clones and 40 clones listed below.

ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 BRACE1000533, BRACE2005457, BRACE2010489, BRACE2014657,
 BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,
 BRACE3003192, BRACE3005499, BRACE3007480, BRACE3009237,
 BRACE3009724, BRACE3009747, BRACE3010428, BRACE3011271,
 BRACE3011421, BRACE3012364, BRACE3013780, BRACE3022769,
 BRACE3026735, BRACE3031838, BRALZ2011796, BRAMY2003008,
 BRAMY2005052, BRAMY2019300, BRAMY2019963, BRAMY2036567,
 BRAMY2037823, BRAMY2040592, BRAMY2047420, BRAMY3002803,
 BRAMY3004224, BRAMY3005091, BRAWH1000127, BRAWH2001395,
 BRAWH2001671, BRAWH2001940, BRAWH2001973, BRAWH2002560,
 BRAWH2002761, BRAWH2005315, BRAWH2007658, BRAWH2010000,
 BRAWH2010084, BRAWH2010536, BRAWH2012162, BRAWH2012326,
 BRAWH2013294, BRAWH2013871, BRAWH2014414, BRAWH2014645,
 BRAWH2014662, BRAWH2014876, BRAWH2014954, BRAWH2016221,
 BRAWH2016439, BRAWH2016702, BRAWH2016724, BRAWH3000078,
 BRAWH3000100, BRAWH3000314, BRAWH3000491, BRAWH3001326,
 BRAWH3001475, BRAWH3001891, BRAWH3002574, BRAWH3002600,
 BRAWH3002819, BRAWH3002821, BRAWH3003522, BRAWH3003555,
 BRAWH3003727, BRAWH3003801, BRAWH3003992, BRAWH3004453,
 BRAWH3004666, BRAWH3005132, BRAWH3005422, BRAWH3005912,

BRAWH3005981, BRAWH3006548, BRAWH3006792, BRAWH3007221,
 BRAWH3007506, BRAWH3007592, BRAWH3007726, BRAWH3007783,
 BRAWH3008341, BRAWH3008697, BRAWH3008931, BRAWH3009297,
 BRCOC2003213, BRCOC2014033, BRCOC2020142, BRHIP2000920,
 5 BRHIP2005719, BRHIP2007741, BRHIP2014228, BRHIP2024146,
 BRHIP3000339, BRHIP3006683, BRHIP3007586, BRHIP3008405,
 BRHIP3018797, BRSSN2000684, BRSSN2003086, BRSSN2004496,
 BRSSN2004719, BRSSN2006892, BRSSN2008549, BRSSN2008797,
 BRSSN2011262, BRSSN2011738, BRSSN2013874, BRSSN2014299,
 10 BRSSN2014424, BRSSN2014556, BRSSN2018581, BRSSN2018925,
 BRSTN2008052, BRSTN2015015, BRSTN2016470, BRTHA1000311,
 BRTHA2003461, BRTHA2008335, BRTHA3002427, BRTHA3003490,
 BRTHA3008520, BRTHA3017848, COLON2001721, CTONG2017500,
 CTONG2028124, CTONG3000657, CTONG3001123, CTONG3009328,
 15 FCBBF2001183, FCBBF3001977, FEBRA2007544, FEBRA2007801,
 FEBRA2020886, FEBRA2024136, FEBRA2025427, FEBRA2028618,
 HCASM2007047, HCHON2000244, HCHON2000626, HCHON2001217,
 HCHON2002676, HCHON2006250, HEART1000074, HHDPC1000118,
 HLUNG2002465, IMR322000127, IMR322002035, KIDNE2006580,
 20 MESAN2006563, MESAN2012054, MESTC1000042, NOVAR2001783,
 NT2NE2006909, NT2RI2008724, NT2RI2012659, NT2RI2014733,
 NT2RI3002892, NT2RI3006284, NT2RI3006673, NT2RI3007543,
 NT2RI3008055, NT2RP7005529, NT2RP7009147, NT2RP7014005,
 NT2RP7017474, OCBBF2001794, OCBBF2006005, OCBBF2006764,
 25 OCBBF2007028, OCBBF2010140, OCBBF2021286, OCBBF2024850,
 OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,
 PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2028914,
 SPLEN2031424, SPLEN2031547, SPLEN2034781, SPLEN2036932,
 30 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4008440, TESOP2002451, TESTI4000014, TESTI4000209,
 TESTI4001100, TESTI4006137, TESTI4008797, TESTI4009286,
 TESTI4010851, TESTI4013817, TESTI4014694, TESTI4021478,
 TESTI4022936, TESTI4024420, TESTI4027821, TESTI4037156,
 35 THYMU2001090, THYMU2033308, THYMU2035735, THYMU2039315,
 THYMU3001234, THYMU3008171, TKIDN2009641, TKIDN2009889,

TKIDN2015788, TRACH1000205, TRACH2001549, TRACH2005811,
 TRACH2006049, TRACH2007834, TRACH2008300, TRACH2025535,
 TRACH3001427, TRACH3002192, TRACH3004721, TRACH3005294,
 TRACH3007479, TRACH3008093, TRACH3009455, UTERU2006115,
 5 UTERU2019706, UTERU2023039, UTERU2026203, UTERU3005230,
 UTERU3007640, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 10 BRHIP2005271, BRHIP3000017, BRTHA2018443, BRTHA3003000,
 CTONG2020374, CTONG2020378, CTONG2024031, FCBBF1000509,
 FEBRA2001990, FEBRA2006519, FEBRA2028516, HCHON2000743,
 IMR322001879, NT2RI2009583, OCBBF2008144, PERIC2007068,
 PUAEN2006335, SPLEN2039379, TESTI2015626, TESTI4001984,
 15 TESTI4008058, TESTI4025268, TESTI4032090, THYMU3000360,
 TLIVE2002046, TRACH3000134, UTERU2021820, UTERU2028734

These genes are involved in Parkinson's disease.

Genes involved in short-term memory and dementia

20 In the brain, the hippocampus is a highly important memory-
 related area. The hippocampus functions to establish a memory
 by judging whether acquired information is necessary, and then
 accumulating the memory in another area of the brain. According
 to clinical findings, patients can retain a new memory for only
 25 about five minutes with an abnormal, or at the worst without a
 hippocampus. Some dementia patients are presumed to have
 hippocampus abnormalities. Thus, genes whose expression levels
 differ between tissues of the whole brain and the hippocampus
 are expected to be involved in memory or dementia. Such genes
 30 can be used to elucidate the mechanism underlying the memory and
 in gene diagnosis. cDNA libraries derived from the hippocampus
 (BRHIP) and from the whole tissues of a normal brain (BRAWH)
 were analyzed and compared (Table 6). Genes whose expression
 levels differed between the two were the 370 clones and 59
 35 clones listed below.

ASTRO1000009, BLADE2001371, BLADE2008398, BNGH42007788,
BRACE1000186, BRACE1000258, BRACE1000533, BRACE2005457,
BRACE2010489, BRACE2014657, BRACE2015058, BRACE2018762,
BRACE2030341, BRACE2035381, BRACE2044286, BRACE2045954,
5 BRACE3000787, BRACE3003192, BRACE3005499, BRACE3007480,
BRACE3009237, BRACE3009724, BRACE3009747, BRACE3010428,
BRACE3011271, BRACE3011421, BRACE3012364, BRACE3018963,
BRACE3022769, BRACE3026735, BRACE3031838, BRALZ2011796,
BRAMY2003008, BRAMY2005052, BRAMY2019300, BRAMY2019963,
10 BRAMY2031317, BRAMY2036567, BRAMY2037823, BRAMY2040592,
BRAMY2044078, BRAMY3002803, BRAMY3004224, BRAMY3005091,
BRAMY3009811, BRAWH1000127, BRAWH2001395, BRAWH2001671,
BRAWH2001940, BRAWH2001973, BRAWH2002560, BRAWH2002761,
BRAWH2005315, BRAWH2007658, BRAWH2010000, BRAWH2010084,
15 BRAWH2010536, BRAWH2012162, BRAWH2012326, BRAWH2013294,
BRAWH2013871, BRAWH2014414, BRAWH2014645, BRAWH2014662,
BRAWH2014876, BRAWH2014954, BRAWH2016221, BRAWH2016439,
BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,
BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
20 BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
BRAWH3003801, BRAWH3003992, BRAWH3004453, BRAWH3004666,
BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
BRAWH3006548, BRAWH3006792, BRAWH3007221, BRAWH3007506,
25 BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2020710,
BRCAN2028355, BRCOC2003213, BRCOC2014033, BRCOC2020142,
BRHIP2000691, BRHIP2000819, BRHIP2000826, BRHIP2000920,
BRHIP2001074, BRHIP2001805, BRHIP2001927, BRHIP2002122,
30 BRHIP2002172, BRHIP2002346, BRHIP2003242, BRHIP2003786,
BRHIP2003917, BRHIP2004312, BRHIP2004359, BRHIP2004814,
BRHIP2004883, BRHIP2005236, BRHIP2005354, BRHIP2005600,
BRHIP2005719, BRHIP2005752, BRHIP2005932, BRHIP2006800,
BRHIP2007616, BRHIP2007741, BRHIP2009340, BRHIP2009414,
35 BRHIP2009474, BRHIP2013699, BRHIP2014228, BRHIP2021615,
BRHIP2022221, BRHIP2024146, BRHIP2024165, BRHIP2026061,

BRHIP2026288, BRHIP2029176, BRHIP2029393, BRHIP3000339,
 BRHIP3000526, BRHIP3001283, BRHIP3006683, BRHIP3007483,
 BRHIP3007586, BRHIP3008183, BRHIP3008313, BRHIP3008344,
 BRHIP3008405, BRHIP3008565, BRHIP3008598, BRHIP3008997,
 5 BRHIP3009099, BRHIP3009448, BRHIP3011241, BRHIP3013765,
 BRHIP3013897, BRHIP3015751, BRHIP3016213, BRHIP3018797,
 BRHIP3020182, BRHIP3024118, BRHIP3024533, BRHIP3024725,
 BRHIP3025161, BRHIP3025702, BRHIP3026097, BRHIP3027137,
 BRHIP3027854, BRSSN2000684, BRSSN2004719, BRSSN2008549,
 10 BRSSN2011738, BRSSN2014299, BRSTN2008052, BRSTN2015015,
 BRSTN2016470, BRSTN2018083, BRTHA1000311, BRTHA2002442,
 BRTHA2008335, BRTHA3000297, BRTHA3001721, BRTHA3002427,
 BRTHA3003490, BRTHA3005046, BRTHA3008520, BRTHA3008778,
 BRTHA3009090, BRTHA3015910, BRTHA3017848, COLON2001721,
 15 CTONG1000087, CTONG1000088, CTONG1000467, CTONG2000042,
 CTONG2008233, CTONG2009423, CTONG2017500, CTONG2019788,
 CTONG2028124, CTONG3000657, CTONG3001123, CTONG3001370,
 CTONG3002412, CTONG3004072, CTONG3008894, CTONG3009239,
 CTONG3009328, DFNES2011499, FCBBF2001183, FCBBF3001977,
 20 FEBRA2000253, FEBRA2007544, FEBRA2007801, FEBRA2008287,
 FEBRA2010719, FEBRA2020886, FEBRA2028618, HCASM2007047,
 HCHON2000028, HCHON2000244, HCHON2000626, HCHON2001217,
 HCHON2002676, HCHON2005921, HCHON2006250, HEART1000074,
 HEART2007031, HHDPC1000118, HLUNG2002465, HLUNG2003003,
 25 IMR322000127, IMR322001380, IMR322002035, KIDNE2005543,
 KIDNE2006580, MESAN2006563, MESAN2012054, MESTC1000042,
 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
 NT2RI2014733, NT2RI2018311, NT2RI3001515, NT2RI3002892,
 NT2RI3004510, NT2RI3005724, NT2RI3006284, NT2RI3006673,
 30 NT2RI3007291, NT2RI3007543, NT2RI3008055, NT2RP7005529,
 NT2RP7009147, NT2RP7014005, NT2RP7017474, OCBBF2001794,
 OCBBF2003819, OCBBF2006005, OCBBF2006151, OCBBF2006764,
 OCBBF2007028, OCBBF2007068, OCBBF2010140, OCBBF2020741,
 OCBBF2021286, OCBBF2024719, OCBBF2024850, OCBBF2028935,
 35 OCBBF2036743, OCBBF2038317, OCBBF3000296, OCBBF3000483,
 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2005930,

PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2010912,
 SPLEN2012624, SPLEN2028914, SPLEN2031424, SPLEN2031547,
 SPLEN2034781, SPLEN2036932, SYNOV2014400, SYNOV4002346,
 SYNOV4002883, SYNOV4007430, SYNOV4008440, TESOP2002451,
 5 TESTI2049246, TESTI4000014, TESTI4000209, TESTI4001100,
 TESTI4006137, TESTI4008797, TESTI4009286, TESTI4010377,
 TESTI4010851, TESTI4010928, TESTI4011161, TESTI4013817,
 TESTI4014159, TESTI4014694, TESTI4014818, TESTI4021478,
 TESTI4022936, TESTI4024420, TESTI4027821, TESTI4037156,
 10 THYMU2001090, THYMU2023967, THYMU2025707, THYMU2031341,
 THYMU2033308, THYMU2035735, THYMU2037226, THYMU2039315,
 THYMU3001234, THYMU3001379, THYMU3004835, THYMU3007137,
 THYMU3008171, TKIDN2009641, TKIDN2009889, TKIDN2015788,
 TRACH1000205, TRACH2001549, TRACH2005811, TRACH2006049,
 15 TRACH2007834, TRACH2008300, TRACH2025535, TRACH3000014,
 TRACH3001427, TRACH3002192, TRACH3004721, TRACH3005294,
 TRACH3007479, TRACH3008093, TRACH3009455, TUTER1000122,
 TUTER2000904, UTERU2004929, UTERU2006115, UTERU2019706,
 UTERU2021163, UTERU2023039, UTERU2026203, UTERU2030213,
 20 UTERU3001572, UTERU3003135, UTERU3005230, UTERU3007640,
 UTERU3009259, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 25 BRHIP2002722, BRHIP2003272, BRHIP2005271, BRHIP2005724,
 BRHIP2006617, BRHIP2008389, BRHIP2012360, BRHIP2017553,
 BRHIP2026877, BRHIP3000017, BRHIP3000240, BRHIP3008314,
 BRHIP3026052, BRTHA2018443, BRTHA3003000, CTONG2020374,
 CTONG2020378, CTONG2024031, CTONG3004726, FCBBF1000509,
 30 FEBRA2001990, FEBRA2006519, FEBRA2028516, HCHON2000743,
 IMR322001879, NT2RI2009583, OCBBF2006987, OCBBF2008144,
 OCBBF2030116, PERIC2007068, PUAEN2006335, SPLEN2039379,
 TESTI2015626, TESTI4000214, TESTI4001984, TESTI4008058,
 TESTI4013894, TESTI4025268, TESTI4025547, TESTI4026207,
 35 TESTI4032090, THYMU3000360, TLIVE2002046, TRACH3000134,
 UTERU2008040, UTERU2021820, UTERU2028734

These genes are involved in memory and dementia.

Genes involved in equilibrium sense and movement function

The cerebellum is the center of equilibrium sense, muscular movement, and motor learning. This area is thought to be involved in motor control, and smooth movements are achieved unconsciously due to cerebellum action. Recent studies have elucidated that the cerebellum participates in not only simple movements but also in establishing higher-order movements such as reading and writing. Thus, genes whose expression levels differ between tissues of the whole brain and the cerebellum are expected to be involved in equilibrium sense or motor function, which can be useful for elucidating the molecular mechanism controlled by the brain. cDNA libraries derived from the cerebellum (BRACE) and from the whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 7). Genes whose expression levels differed between the two were the 488 clones and 66 clones listed below.

ADRL2009146, ADRL2012038, ASTRO1000009, ASTRO2003960,
BLADE1000176, BLADE2004089, BLADE2008398, BRACE1000186,
BRACE1000258, BRACE1000533, BRACE1000572, BRACE2003639,
BRACE2005457, BRACE2006319, BRACE2008594, BRACE2010489,
BRACE2011747, BRACE2014306, BRACE2014475, BRACE2014657,
BRACE2015058, BRACE2015314, BRACE2016981, BRACE2018762,
BRACE2024627, BRACE2026836, BRACE2027258, BRACE2027970,
BRACE2028970, BRACE2029112, BRACE2029849, BRACE2030326,
BRACE2030341, BRACE2030884, BRACE2031154, BRACE2031389,
BRACE2031527, BRACE2031531, BRACE2031899, BRACE2032044,
BRACE2032329, BRACE2032385, BRACE2032538, BRACE2032823,
BRACE2033720, BRACE2035381, BRACE2035441, BRACE2036005,
BRACE2036096, BRACE2036830, BRACE2036834, BRACE2037847,
BRACE2038114, BRACE2038329, BRACE2038551, BRACE2039249,
BRACE2039327, BRACE2039475, BRACE2039734, BRACE2040138,
BRACE2040325, BRACE2041009, BRACE2041200, BRACE2041264,
BRACE2042550, BRACE2043142, BRACE2043248, BRACE2043349,
BRACE2043665, BRACE2044286, BRACE2044816, BRACE2044949,

BRACE2045300, BRACE2045428, BRACE2045596, BRACE2045772,
BRACE2045947, BRACE2045954, BRACE2046251, BRACE2046295,
BRACE2047011, BRACE2047350, BRACE2047377, BRACE2047385,
BRACE3000071, BRACE3000697, BRACE3000787, BRACE3000840,
5 BRACE3000973, BRACE3001002, BRACE3001217, BRACE3001391,
BRACE3001595, BRACE3001754, BRACE3002298, BRACE3002390,
BRACE3002508, BRACE3003004, BRACE3003192, BRACE3003595,
BRACE3003698, BRACE3004058, BRACE3004113, BRACE3004150,
BRACE3004358, BRACE3004435, BRACE3004772, BRACE3004783,
10 BRACE3004843, BRACE3004880, BRACE3005145, BRACE3005225,
BRACE3005430, BRACE3005499, BRACE3006185, BRACE3006226,
BRACE3006462, BRACE3006872, BRACE3007322, BRACE3007472,
BRACE3007480, BRACE3007559, BRACE3007625, BRACE3007642,
BRACE3007767, BRACE3008036, BRACE3008092, BRACE3008137,
15 BRACE3008384, BRACE3008720, BRACE3008772, BRACE3009090,
BRACE3009237, BRACE3009297, BRACE3009377, BRACE3009574,
BRACE3009701, BRACE3009708, BRACE3009724, BRACE3009747,
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25 BRACE3020594, BRACE3022769, BRACE3023912, BRACE3024073,
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30 BRACE3045033, BRALZ2011796, BRAMY2003008, BRAMY2005052,
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BRAMY2040592, BRAMY2044078, BRAMY2047420, BRAMY3002620,
BRAMY3002803, BRAMY3004224, BRAMY3005091, BRAMY3005932,
35 BRAMY4000229, BRAWH1000127, BRAWH2001395, BRAWH2001671,
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 BRAWH2013871, BRAWH2014414, BRAWH2014645, BRAWH2014662,
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 5 BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,
 BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
 BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
 BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
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 10 BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
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 BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
 BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2009432,
 BRCAN2010376, BRCAN2015371, BRCAN2020710, BRCOC2003213,
 15 BRCOC2007034, BRCOC2014033, BRCOC2020142, BRHIP2000920,
 BRHIP2004359, BRHIP2005719, BRHIP2005752, BRHIP2007741,
 BRHIP2013699, BRHIP2014228, BRHIP2024146, BRHIP3000339,
 BRHIP3006683, BRHIP3007586, BRHIP3008313, BRHIP3008405,
 BRHIP3018797, BRSSN2000684, BRSSN2006892, BRSSN2011262,
 20 BRSSN2011738, BRSSN2014299, BRSTN2008052, BRSTN2010750,
 BRSTN2015015, BRSTN2016470, BRTHA1000311, BRTHA2008335,
 BRTHA2008955, BRTHA2011194, BRTHA3001721, BRTHA3002427,
 BRTHA3003490, BRTHA3008520, BRTHA3009090, BRTHA3017848,
 COLON2001721, CTONG2008233, CTONG2017500, CTONG2028124,
 25 CTONG3000657, CTONG3001123, CTONG3005813, CTONG3008894,
 CTONG3009328, DFNES2011499, FCBBF2001183, FCBBF3001977,
 FEBRA2006396, FEBRA2007544, FEBRA2007708, FEBRA2007801,
 FEBRA2008287, FEBRA2020886, FEBRA2021966, FEBRA2026984,
 FEBRA2028618, HCASM2007047, HCHON2000244, HCHON2000626,
 30 HCHON2001217, HCHON2002676, HCHON2005921, HCHON2006250,
 HEART1000074, HHDPC1000118, HLUNG2002465, IMR322000127,
 IMR322001380, IMR322002035, KIDNE2000665, KIDNE2006580,
 MESAN2006563, MESAN2012054, MESTC1000042, NB9N41000340,
 NESOP2001752, NOVAR2001783, NT2NE2006909, NT2RI2005166,
 35 NT2RI2008724, NT2RI2012659, NT2RI2014733, NT2RI2019751,
 NT2RI3002892, NT2RI3003382, NT2RI3004510, NT2RI3005724,

NT2RI3006284, NT2RI3006673, NT2RI3007291, NT2RI3007543,
 NT2RI3008055, NT2RP7004123, NT2RP7005529, NT2RP7009147,
 NT2RP7010599, NT2RP7014005, NT2RP7017474, NTONG2005969,
 OCBBF2001794, OCBBF2003819, OCBBF2006005, OCBBF2006151,
 5 OCBBF2006764, OCBBF2007028, OCBBF2010140, OCBBF2020343,
 OCBBF2020741, OCBBF2021286, OCBBF2022351, OCBBF2024850,
 OCBBF2025527, OCBBF2028935, OCBBF2036743, OCBBF2038317,
 OCBBF3000483, OCBBF3007516, OCBBF3008230, PEBLM2004666,
 PERIC2000889, PLACE6001185, PUAEN2002489, PUAEN2005930,
 10 PUAEN2006701, PUAEN2007044, PUAEN2009655, SPLEN2010912,
 SPLEN2012624, SPLEN2027268, SPLEN2028914, SPLEN2031424,
 SPLEN2031547, SPLEN2034781, SPLEN2036932, SPLEN2037194,
 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4007671, SYNOV4008440, TESOP2002273, TESOP2002451,
 15 TESOP2002950, TESTI1000330, TESTI4000014, TESTI4000209,
 TESTI4000349, TESTI4001100, TESTI4001561, TESTI4006137,
 TESTI4008797, TESTI4009286, TESTI4010851, TESTI4011161,
 TESTI4013675, TESTI4013817, TESTI4014159, TESTI4014306,
 TESTI4014694, TESTI4021478, TESTI4022936, TESTI4024420,
 20 TESTI4027821, TESTI4037156, TESTI4046819, THYMU2001090,
 THYMU2016523, THYMU2023967, THYMU2030264, THYMU2033308,
 THYMU2035735, THYMU2039315, THYMU2039780, THYMU3001083,
 THYMU3001234, THYMU3003309, THYMU3006485, THYMU3008171,
 TKIDN2009641, TKIDN2009889, TKIDN2015788, TRACH1000205,
 25 TRACH2001549, TRACH2005811, TRACH2006049, TRACH2007834,
 TRACH2008300, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004721, TRACH3005294, TRACH3006038, TRACH3006412,
 TRACH3007479, TRACH3008093, TRACH3009455, TUTER2000904,
 UTERU2002410, UTERU2006115, UTERU2007520, UTERU2019706,
 30 UTERU2023039, UTERU2026203, UTERU3000226, UTERU3001572,
 UTERU3005230, UTERU3005460, UTERU3005970, UTERU3006308,
 UTERU3007419, UTERU3007640, UTERU3007913, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2002589, BRACE2003609,
 BRACE2009318, BRACE2011677, BRACE2029396, BRACE2037299,
 35 BRACE2039823, BRACE2039832, BRACE2043105, BRACE3001058,
 BRACE3001113, BRACE3003026, BRACE3003053, BRACE3009127,

BRACE3010076, BRACE3015829, BRACE3021148, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRCOC2019841, BRHIP2005271, BRHIP3000017, BRHIP3000240,
 5 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000743, IMR322001879, NT2RI2009583,
 NT2RP8000521, OCBBF2008144, OCBBF2011669, PERIC2007068,
 PUAEN2006335, SPLEN2039379, SYNOV2021953, TESTI2015626,
 10 TESTI4001984, TESTI4008058, TESTI4013894, TESTI4025268,
 TESTI4032090, THYMU2004284, THYMU2040925, THYMU3000360,
 TLIVE2002046, TRACH3000134, UTERU2008040, UTERU2011220,
 UTERU2021820, UTERU2028734

These genes are involved in equilibrium sense or motor
 15 function.

Genes involved in signaling from sensory organs

The thalamus is an area which comprises many neurons
 strongly connected to the cerebrum, and which transmits sensory
 20 information from the spinal cord or such to the responsible area
 of the cerebrum. The thalamus also controls the direction of
 movement from the cerebrum. For example, the thalamus resolves
 vision into the elements of size, shape, and color, and resolves
 sound into volume and sweetness or harshness to the ear, and
 25 then transmits this information to the sensory area of the
 cerebral cortex. Thus, genes whose expression levels differ
 between tissues of the whole brain and the thalamus are expected
 to be involved in signaling from sensory organs. These genes
 can be used to elucidate the molecular mechanism underlying
 30 signaling controlled by the brain. cDNA libraries derived from
 the thalamus (BRTHA) and from whole tissues of a normal brain
 (BRAWH) were analyzed and compared (Table 8). Genes whose
 expression levels differed between the two were the 412 clones
 and 56 clones listed below.

35 ASTRO1000009, ASTRO3000482, BLADE2008398, BRACE1000186,
 BRACE1000258, BRACE1000533, BRACE2005457, BRACE2010489,

BRACE2014306, BRACE2014657, BRACE2015058, BRACE2031154,
BRACE2035381, BRACE2044286, BRACE2045954, BRACE3000787,,
BRACE3003192, BRACE3005499, BRACE3007480, BRACE3008384,
BRACE3009237, BRACE3009724, BRACE3009747, BRACE3010397,
5 BRACE3010428, BRACE3011271, BRACE3011421, BRACE3012364,
BRACE3022769, BRACE3026735, BRACE3027478, BRACE3031838,
BRALZ2011796, BRAMY2003008, BRAMY2005052, BRAMY2019300,
BRAMY2019963, BRAMY2028914, BRAMY2031317, BRAMY2036567,
BRAMY2037823, BRAMY2040592, BRAMY2044078, BRAMY3002803,
10 BRAMY3004224, BRAMY3005091, BRAMY4000229, BRAWH1000127,
BRAWH2001395, BRAWH2001671, BRAWH2001940, BRAWH2001973,
BRAWH2002560, BRAWH2002761, BRAWH2005315, BRAWH2007658,
BRAWH2010000, BRAWH2010084, BRAWH2010536, BRAWH2012162,
BRAWH2012326, BRAWH2013294, BRAWH2013871, BRAWH2014414,
15 BRAWH2014645, BRAWH2014662, BRAWH2014876, BRAWH2014954,
BRAWH2016221, BRAWH2016439, BRAWH2016702, BRAWH2016724,
BRAWH3000078, BRAWH3000100, BRAWH3000314, BRAWH3000491,
BRAWH3001326, BRAWH3001475, BRAWH3001891, BRAWH3002574,
BRAWH3002600, BRAWH3002819, BRAWH3002821, BRAWH3003522,
20 BRAWH3003555, BRAWH3003727, BRAWH3003801, BRAWH3003992,
BRAWH3004453, BRAWH3004666, BRAWH3005132, BRAWH3005422,
BRAWH3005912, BRAWH3005981, BRAWH3006548, BRAWH3006792,
BRAWH3007221, BRAWH3007506, BRAWH3007592, BRAWH3007726,
BRAWH3007783, BRAWH3008341, BRAWH3008697, BRAWH3008931,
25 BRAWH3009297, BRCAN2006297, BRCOC2003213, BRCOC2014033,
BRCOC2020142, BRHIP2000819, BRHIP2000920, BRHIP2005719,
BRHIP2007741, BRHIP2009474, BRHIP2013699, BRHIP2014228,
BRHIP2022221, BRHIP2024146, BRHIP3000339, BRHIP3006683,
BRHIP3007586, BRHIP3008405, BRHIP3018797, BRSSN2000684,
30 BRSSN2008549, BRSSN2008797, BRSSN2011738, BRSSN2014299,
BRSTN2004863, BRSTN2008052, BRSTN2015015, BRSTN2016470,
BRTHA1000311, BRTHA2000855, BRTHA2001462, BRTHA2002115,
BRTHA2002281, BRTHA2002376, BRTHA2002442, BRTHA2002493,
BRTHA2002608, BRTHA2002808, BRTHA2003030, BRTHA2003110,
35 BRTHA2003116, BRTHA2003461, BRTHA2004821, BRTHA2004978,
BRTHA2005579, BRTHA2005956, BRTHA2006075, BRTHA2006146,

BRTHA2006194, BRTHA2007122, BRTHA2007422, BRTHA2007603,
 BRTHA2008316, BRTHA2008335, BRTHA2008527, BRTHA2008535,
 BRTHA2008955, BRTHA2009311, BRTHA2009846, BRTHA2009972,
 BRTHA2010073, BRTHA2010608, BRTHA2010884, BRTHA2010907,
 5 BRTHA2011194, BRTHA2011351, BRTHA2011500, BRTHA2011641,
 BRTHA2012392, BRTHA2012562, BRTHA2012980, BRTHA2013262,
 BRTHA2013460, BRTHA2013707, BRTHA2014792, BRTHA2014828,
 BRTHA2015406, BRTHA2015478, BRTHA2015696, BRTHA2015878,
 BRTHA2016215, BRTHA2016496, BRTHA2016543, BRTHA2017353,
 10 BRTHA2017985, BRTHA2018165, BRTHA2018344, BRTHA2018591,
 BRTHA2018624, BRTHA2018707, BRTHA2019014, BRTHA2019022,
 BRTHA2019048, BRTHA3000273, BRTHA3000297, BRTHA3000633,
 BRTHA3001721, BRTHA3002401, BRTHA3002427, BRTHA3002933,
 BRTHA3003074, BRTHA3003343, BRTHA3003449, BRTHA3003474,
 15 BRTHA3003490, BRTHA3004475, BRTHA3005046, BRTHA3006856,
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 BRTHA3008143, BRTHA3008310, BRTHA3008386, BRTHA3008520,
 BRTHA3008778, BRTHA3009037, BRTHA3009090, BRTHA3009291,
 BRTHA3010366, BRTHA3013884, BRTHA3015815, BRTHA3015910,
 20 BRTHA3016845, BRTHA3016917, BRTHA3017047, BRTHA3017589,
 BRTHA3017848, BRTHA3018514, BRTHA3018617, BRTHA3018656,
 BRTHA3019105, COLON2001721, CTONG1000087, CTONG2008233,
 CTONG2017500, CTONG2019788, CTONG2023021, CTONG2028124,
 CTONG3000657, CTONG3001123, CTONG3008894, CTONG3009028,
 25 CTONG3009239, CTONG3009328, FCBBF2001183, FCBBF3001977,
 FCBBF3021576, FEBRA2007544, FEBRA2007801, FEBRA2008287,
 FEBRA2008360, FEBRA2020886, FEBRA2028618, HCASM2007047,
 HCHON2000028, HCHON2000212, HCHON2000244, HCHON2000626,
 HCHON2001084, HCHON2001217, HCHON2002676, HCHON2005921,
 30 HCHON2006250, HEART1000074, HEART2007031, HHDPC1000118,
 HLUNG2001996, HLUNG2002465, IMR322000127, IMR322001380,
 IMR322002035, KIDNE2002252, KIDNE2005543, KIDNE2006580,
 KIDNE2011314, MESAN2006563, MESAN2012054, MESTC1000042,
 NOVAR2001783, NT2NE2006909, NT2RI2008724, NT2RI2012659,
 35 NT2RI2014733, NT2RI3002842, NT2RI3002892, NT2RI3005403,
 NT2RI3006284, NT2RI3006673, NT2RI3007543, NT2RI3008055,

NT2RP7004123, NT2RP7005529, NT2RP7009147, NT2RP7014005,
 NT2RP7017474, NTONG2005969, NTONG2008088, OCBBF2001794,
 OCBBF2006005, OCBBF2006764, OCBBF2007028, OCBBF2010140,
 OCBBF2020639, OCBBF2021286, OCBBF2024719, OCBBF2024850,
 5 OCBBF2028935, OCBBF2036743, OCBBF2038317, OCBBF3000483,
 OCBBF3008230, PEBLM2004666, PLACE6001185, PUAEN2002489,
 PUAEN2005930, PUAEN2006701, PUAEN2007044, PUAEN2009655,
 RECTM2001347, SKMUS2000757, SPLEN2006122, SPLEN2010912,
 SPLEN2025491, SPLEN2028914, SPLEN2031424, SPLEN2031547,
 10 SPLEN2032154, SPLEN2034781, SPLEN2036821, SPLEN2036932,
 SYNOV1000374, SYNOV2014400, SYNOV4002346, SYNOV4002883,
 SYNOV4007430, SYNOV4007671, SYNOV4008440, TESOP2002451,
 TESTI2049246, TESTI4000014, TESTI4000209, TESTI4001100,
 TESTI4002290, TESTI4006137, TESTI4008797, TESTI4009286,
 15 TESTI4010851, TESTI4012702, TESTI4013817, TESTI4014159,
 TESTI4014694, TESTI4021478, TESTI4022936, TESTI4024420,
 TESTI4027821, TESTI4037156, THYMU2001090, THYMU2025707,
 THYMU2032825, THYMU2033308, THYMU2033787, THYMU2035735,
 THYMU2039315, THYMU2040975, THYMU3001234, THYMU3001379,
 20 THYMU3004835, THYMU3008171, TKIDN2009641, TKIDN2009889,
 TKIDN2015788, TLIVE2001327, TRACH1000205, TRACH2001549,
 TRACH2005811, TRACH2006049, TRACH2007834, TRACH2008300,
 TRACH2023299, TRACH2025535, TRACH3001427, TRACH3002192,
 TRACH3004068, TRACH3004721, TRACH3005294, TRACH3007479,
 25 TRACH3008093, TRACH3009455, TSTOM1000135, TUTER2000904,
 UTERU2002410, UTERU2006115, UTERU2019706, UTERU2019940,
 UTERU2023039, UTERU2023175, UTERU2026203, UTERU2030280,
 UTERU3000899, UTERU3001571, UTERU3001572, UTERU3004709,
 UTERU3005230, UTERU3005907, UTERU3007640, UTERU3009871
 30 ADRGL2000042, BLADE2006830, BRACE2003609, BRAMY3004800,
 BRAWH1000369, BRAWH2006207, BRAWH2006395, BRAWH2008993,
 BRAWH2009393, BRAWH2010552, BRAWH3007441, BRAWH3009017,
 BRHIP2005271, BRHIP3000017, BRTHA2002133, BRTHA2002702,
 BRTHA2007060, BRTHA2010033, BRTHA2011321, BRTHA2013426,
 35 BRTHA2013610, BRTHA2016318, BRTHA2017364, BRTHA2017972,
 BRTHA2018011, BRTHA2018443, BRTHA3000296, BRTHA3003000,

BRTHA3008826, CTONG2008721, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 FEBRA2028516, HCHON2000743, HSYRA2005628, IMR322001879,
 NT2RI2009583, OCBBF2008144, PERIC2007068, PUAEN2006335,
 5 SPLEN2016932, SPLEN2039379, SYNOV2006620, TESTI4001984,
 TESTI4008058, TESTI4025268, TESTI4032090, THYMU3000360,
 TLIVE2002046, TRACH3000134, UTERU2021820, UTERU2028734

These genes are involved in signaling from sensory organs.

10 Genes involved in emotional reaction

The amygdala is the center of emotion in the brain. Information passing through the amygdala induces an emotional reaction, for example, panic or fear. When a strong fear reaction is produced due to the emotional evaluation of stimulus
 15 in the amygdala, the amygdala transmits an alert signal to each area of the brain. This results in various reactions such as sweating palms, palpitation, elevated blood pressure, and rapid secretion of adrenaline. In other words, the amygdala transmits signals which cause the body to be on the alert and is a tissue
 20 involved in a kind of defense instinct. Thus, genes whose expression levels differ between tissues of the whole brain and the amygdala are expected to be involved in emotional reaction. Such genes can be used to elucidate the molecular mechanism underlying emotional reaction, fear, or panic. cDNA libraries
 25 derived from the amygdale (BRAMY) and from whole tissues of a normal brain (BRAWH) were analyzed and compared (Table 9). Genes whose expression levels differed between the two were the 383 clones and 55 clones listed below.

ASTRO1000009, BLADE2008398, BRACE1000186, BRACE1000258,
 30 BRACE1000533, BRACE2005457, BRACE2006319, BRACE2010489,
 BRACE2014657, BRACE2015058, BRACE2027258, BRACE2030341,
 BRACE2031389, BRACE2035381, BRACE2044286, BRACE2045954,
 BRACE3000787, BRACE3000973, BRACE3003192, BRACE3005499,
 BRACE3007480, BRACE3008036, BRACE3009237, BRACE3009724,
 35 BRACE3009747, BRACE3010428, BRACE3011271, BRACE3011421,
 BRACE3012364, BRACE3013780, BRACE3022769, BRACE3026735,

BRACE3027478, BRACE3031838, BRALZ2011796, BRAMY2001473,
 BRAMY2003008, BRAMY2004771, BRAMY2005052, BRAMY2017528,
 BRAMY2019300, BRAMY2019963, BRAMY2019985, BRAMY2020058,
 BRAMY2020270, BRAMY2021498, BRAMY2028856, BRAMY2028914,
 5 BRAMY2029602, BRAMY2030098, BRAMY2030109, BRAMY2030702,
 BRAMY2030703, BRAMY2030799, BRAMY2031317, BRAMY2031377,
 BRAMY2031442, BRAMY2032014, BRAMY2032242, BRAMY2032317,
 BRAMY2033003, BRAMY2033116, BRAMY2033267, BRAMY2033594,
 BRAMY2034185, BRAMY2034920, BRAMY2034993, BRAMY2036387,
 10 BRAMY2036396, BRAMY2036567, BRAMY2036699, BRAMY2036913,
 BRAMY2037823, BRAMY2038100, BRAMY2038484, BRAMY2038846,
 BRAMY2038904, BRAMY2039872, BRAMY2040478, BRAMY2040592,
 BRAMY2041261, BRAMY2041378, BRAMY2041542, BRAMY2042612,
 BRAMY2042641, BRAMY2042760, BRAMY2042918, BRAMY2044078,
 15 BRAMY2044246, BRAMY2045036, BRAMY2046478, BRAMY2046742,
 BRAMY2046989, BRAMY2047169, BRAMY2047420, BRAMY2047676,
 BRAMY2047746, BRAMY2047751, BRAMY2047765, BRAMY2047884,
 BRAMY3000206, BRAMY3000213, BRAMY3001401, BRAMY3001794,
 BRAMY3002312, BRAMY3002620, BRAMY3002803, BRAMY3002805,
 20 BRAMY3004224, BRAMY3004672, BRAMY3004900, BRAMY3004919,
 BRAMY3005091, BRAMY3005932, BRAMY3006297, BRAMY3007206,
 BRAMY3007609, BRAMY3008466, BRAMY3008505, BRAMY3008650,
 BRAMY3009811, BRAMY3010411, BRAMY4000095, BRAMY4000229,
 BRAMY4000277, BRAWH1000127, BRAWH2001395, BRAWH2001671,
 25 BRAWH2001940, BRAWH2001973, BRAWH2002560, BRAWH2002761,
 BRAWH2005315, BRAWH2007658, BRAWH2010000, BRAWH2010084,
 BRAWH2010536, BRAWH2012162, BRAWH2012326, BRAWH2013294,
 BRAWH2013871, BRAWH2014414, BRAWH2014645, BRAWH2014662,
 BRAWH2014876, BRAWH2014954, BRAWH2016221, BRAWH2016439,
 30 BRAWH2016702, BRAWH2016724, BRAWH3000078, BRAWH3000100,
 BRAWH3000314, BRAWH3000491, BRAWH3001326, BRAWH3001475,
 BRAWH3001891, BRAWH3002574, BRAWH3002600, BRAWH3002819,
 BRAWH3002821, BRAWH3003522, BRAWH3003555, BRAWH3003727,
 BRAWH3003801, BRAWH3003992, BRAWH3004453, BRAWH3004666,
 35 BRAWH3005132, BRAWH3005422, BRAWH3005912, BRAWH3005981,
 BRAWH3006548, BRAWH3006792, BRAWH3007221, BRAWH3007506,

BRAWH3007592, BRAWH3007726, BRAWH3007783, BRAWH3008341,
 BRAWH3008697, BRAWH3008931, BRAWH3009297, BRCAN2014881,
 BRCAN2017717, BRCOC2000670, BRCOC2003213, BRCOC2014033,
 BRCOC2020142, BRHIP2000920, BRHIP2005719, BRHIP2007741,
 5 BRHIP2014228, BRHIP2024146, BRHIP2026061, BRHIP3000339,
 BRHIP3001283, BRHIP3006683, BRHIP3007586, BRHIP3008405,
 BRHIP3018797, BRSSN2000684, BRSSN2004496, BRSSN2011738,
 BRSSN2014299, BRSTN2008052, BRSTN2010750, BRSTN2015015,
 BRSTN2016470, BRTHA1000311, BRTHA2008335, BRTHA2011641,
 10 BRTHA3001721, BRTHA3002427, BRTHA3003490, BRTHA3004475,
 BRTHA3008520, BRTHA3009090, BRTHA3017848, COLON2001721,
 CTONG1000087, CTONG2008233, CTONG2017500, CTONG2028124,
 CTONG3000657, CTONG3001123, CTONG3008894, CTONG3009239,
 CTONG3009328, FCBBF2001183, FCBBF3001977, FEBRA2007544,
 15 FEBRA2007801, FEBRA2008287, FEBRA2010719, FEBRA2020886,
 FEBRA2025427, FEBRA2028618, HCASM2007047, HCHON2000244,
 HCHON2000626, HCHON2001217, HCHON2002676, HCHON2006250,
 HCHON2008112, HEART1000074, HHDP1000118, HLUNG2002465,
 HSYRA2009075, IMR322000127, IMR322001380, IMR322002035,
 20 KIDNE2000665, KIDNE2006580, MESAN2006563, MESAN2012054,
 MESAN2015515, MESTC1000042, NOVAR2001783, NT2NE2005890,
 NT2NE2006909, NT2RI2008724, NT2RI2012659, NT2RI2014733,
 NT2RI3001515, NT2RI3002892, NT2RI3005724, NT2RI3006284,
 NT2RI3006673, NT2RI3007543, NT2RI3008055, NT2RP7005529,
 25 NT2RP7009147, NT2RP7014005, NT2RP7017474, NTONG2005969,
 OCBBF1000254, OCBBF2001794, OCBBF2006005, OCBBF2006764,
 OCBBF2007028, OCBBF2007114, OCBBF2010140, OCBBF2021286,
 OCBBF2023162, OCBBF2024850, OCBBF2028935, OCBBF2035214,
 OCBBF2036743, OCBBF2038317, OCBBF3000483, OCBBF3008230,
 30 PEBLM2004666, PERIC2000889, PERIC2003720, PLACE6001185,
 PUAEN2005930, PUAEN2006701, PUAEN2007044, PUAEN2009174,
 PUAEN2009655, SKNMC2002402, SKNSH2000482, SPLEN2001599,
 SPLEN2002467, SPLEN2028914, SPLEN2029912, SPLEN2031424,
 SPLEN2031547, SPLEN2034781, SPLEN2036932, SPLEN2038345,
 35 SYNOV2014400, SYNOV4002346, SYNOV4002883, SYNOV4007430,
 SYNOV4007671, SYNOV4008440, TESOP2002451, TESTI2009474,

TESTI4000014, TESTI4000209, TESTI4001100, TESTI4006137,
 TESTI4008797, TESTI4009286, TESTI4010851, TESTI4013817,
 TESTI4014159, TESTI4014694, TESTI4021478, TESTI4022936,
 TESTI4024420, TESTI4027821, TESTI4029836, TESTI4037156,
 5 TESTI4037188, THYMU2001090, THYMU2014353, THYMU2033308,
 THYMU2035735, THYMU2037226, THYMU2039315, THYMU3001234,
 THYMU3001379, THYMU3004835, THYMU3008171, TKIDN2009641,
 TKIDN2009889, TKIDN2015788, TLIVE2004320, TRACH1000205,
 TRACH2001549, TRACH2001684, TRACH2005811, TRACH2006049,
 10 TRACH2007834, TRACH2008300, TRACH2025344, TRACH2025535,
 TRACH2025911, TRACH3001427, TRACH3002192, TRACH3004068,
 TRACH3004721, TRACH3005294, TRACH3007479, TRACH3008093,
 TRACH3009455, TUTER2000904, UTERU2002410, UTERU2004929,
 UTERU2006115, UTERU2007520, UTERU2019706, UTERU2023039,
 15 UTERU2026203, UTERU3001572, UTERU3001766, UTERU3005230,
 UTERU3007640, UTERU3009517, UTERU3009871
 ADRGL2000042, BLADE2006830, BRACE2003609, BRACE2039823,
 BRAMY2019111, BRAMY2035070, BRAMY2035449, BRAMY2035718,
 BRAMY2038516, BRAMY2039341, BRAMY2040159, BRAMY2041434,
 20 BRAWH2045471, BRAWH2004800, BRAWH1000369, BRAWH2006207,
 BRAWH2006395, BRAWH2008993, BRAWH2009393, BRAWH2010552,
 BRAWH3007441, BRAWH3009017, BRHIP2005271, BRHIP3000017,
 BRTHA2018443, BRTHA3003000, CTONG2020374, CTONG2020378,
 CTONG2024031, FCBBF1000509, FEBRA2001990, FEBRA2006519,
 25 FEBRA2028516, HCHON2000508, HCHON2000743, IMR322001879,
 NT2RI2009583, OCBBF2008144, PERIC2007068, PUAEN2006335,
 SPLEN2039379, TESTI2015626, TESTI2026647, TESTI4001984,
 TESTI4008058, TESTI4013894, TESTI4025268, TESTI4032090,
 THYMU3000360, TKIDN2018926, TLIVE2002046, TRACH3000134,
 30 UTERU2008040, UTERU2021820, UTERU2028734

These genes are involved in emotional reaction.

Cancer-related genes

35 Cancer tissues are assumed to express a distinct set of
 genes distinct from normal tissues, and thus expression of these
 genes can contribute to carcinogenesis in tissues and cells.

Thus, genes whose expression patterns in cancer tissues differ from those in normal tissues are cancer-related genes. A search was carried out for genes whose expression levels in cancer tissues differed from those in normal tissues.

5 The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) (Table 10) showed that the genes whose expression levels differed between the two were 35 and four clones as described below.

10 ASTRO2002842, BRACE3016884, BRSSN2011262, BRTHA2008335,
HCHON2000244, HCHON2006250, HEART1000010, MESAN2012054,
NT2RP7000466, NT2RP7009147, OCBBF2021020, PEBLM2002749,
PEBLM2004666, SPLEN2001599, SPLEN2031547, STOMA1000189,
TBAES2001171, TBAES2001220, TBAES2001229, TBAES2001258,
15 TBAES2001492, TBAES2001751, TBAES2002197, TBAES2003550,
TBAES2004055, TBAES2005157, TBAES2005543, TBAES2006568,
TBAES2007964, TESTI4000014, TESTI4037156, TRACH3002192,
TRACH3004068, TSTOM2000553, UTERU2002410
BRAWH2006395, NT2RI2009583, STOMA2004893, TBAES2000932

20 The result of comparative analysis of cDNA libraries derived from cervical tumor (TCERX) and normal cervical duct (CERVX) (Table 11) showed that the genes whose expression levels differed between the two were twelve and two clones as described below.

25 BLADE2007666, BRAMY2047420, BRCAN2007409, BRSTN2016470,
CERVX1000042, CERVX2002006, MESAN2006563, PROST2018090,
TCERX2000613, TESTI4037156, THYMU2031341, UTERU2004688
CERVX2002013, NT2RI2009583

30 The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) (Table 12) showed that the genes whose expression levels were different between the two were 24 and four clones as described below.

BRACE3015027, BRAMY2040592, BRSTN2016470, COLON1000030,
COLON2000470, COLON2000568, COLON2001721, COLON2002443,
35 COLON2002520, COLON2003043, COLON2004478, COLON2005126,
COLON2005772, COLON2006282, COLON2009499, OCBBF2028935,

PLACE7000514, RECTM2000433, SYNOV4007671, TCOLN2002278,
 TESTI2052693, TESTI4037156, THYMU2031368, TRACH2025535
 CTONG1000113, NT2RI2009583, NT2RI2018448, TESTI2015626

The result of comparative analysis of cDNA libraries
 5 derived from esophageal tumor (TESOP) and normal esophagus
 (NESOP) (Table 13) showed that the genes whose expression levels
 were different between the two were 56 and ten clones as
 described below.

BRACE2030341, BRAMY2047420, BRHIP2003917, BRTHA2003461,
 10 CTONG2013178, D3OST3000169, FEBRA2025427, HCHON2000244,
 HHDPC1000118, NESOP2000744, NESOP2001433, NESOP2001656,
 NESOP2001694, NESOP2001752, NESOP2002738, NT2RI3006284,
 NT2RP7009147, PLACE6019932, SYNOV2005216, TESOP1000127,
 TESOP2000801, TESOP2001122, TESOP2001166, TESOP2001345,
 15 TESOP2001605, TESOP2001818, TESOP2001849, TESOP2001865,
 TESOP2001953, TESOP2002273, TESOP2002451, TESOP2002489,
 TESOP2002539, TESOP2002950, TESOP2003273, TESOP2003753,
 TESOP2004114, TESOP2005285, TESOP2005485, TESOP2005579,
 TESOP2006041, TESOP2006060, TESOP2006068, TESOP2006670,
 20 TESOP2006746, TESOP2007052, TESOP2007262, TESOP2007636,
 TESOP2007688, TESOP2009121, TESOP2009555, TESTI4009286,
 TESTI4010851, THYMU2040975, TRACH2005811, UTERU2023175
 CTONG2016942, NT2RI2009583, TESOP2000390, TESOP2001796,
 TESOP2005199, TESOP2006398, TESOP2006865, TESOP2007384,
 25 TESTI2015626, TRACH2000862

The result of comparative analysis of cDNA libraries
 derived from kidney tumor (TKIDN) and normal kidney (KIDNE)
 (Table 14) showed that the genes whose expression levels were
 different between the two were 96 and 13 clones as described
 30 below.

ASTRO2018373, BRACE1000186, BRACE2014306, BRACE2015058,
 BRACE2016981, BRACE2043665, BRACE3008036, BRACE3010428,
 BRACE3022769, BRAMY2019963, BRAMY2044078, BRAWH1000127,
 BRAWH2001395, BRAWH2001671, BRAWH2013294, BRAWH2014645,
 35 BRHIP2024146, BRHIP3000339, BRSSN2000684, BRSSN2004719,
 BRSSN2018581, BRSTN2016470, BRTHA1000311, BRTHA3002427,

CTONG1000087, CTONG2028124, CTONG3000657, CTONG3008894,
 FCBBF2001183, FEBRA2008287, HCASM2001301, HCHON2000028,
 HCHON2000244, HEART1000074, HHDPC1000118, HSYRA2008376,
 KIDNE1000064, KIDNE2000665, KIDNE2000722, KIDNE2000832,
 5 KIDNE2000846, KIDNE2001361, KIDNE2001847, KIDNE2002252,
 KIDNE2002991, KIDNE2003837, KIDNE2005543, KIDNE2006580,
 KIDNE2010264, KIDNE2011314, KIDNE2011532, KIDNE2011635,
 KIDNE2012945, KIDNE2013095, NESOP2001656, NTONG2005969,
 PEBLM2004666, SKMUS2000757, STOMA1000189, SYNOV4007671,
 10 TBAES2001258, TESTI4000014, TESTI4001100, TESTI4012702,
 TESTI4046819, THYMU2032014, TKIDN2000701, TKIDN2002424,
 TKIDN2002632, TKIDN2003044, TKIDN2004386, TKIDN2005934,
 TKIDN2005947, TKIDN2006525, TKIDN2006852, TKIDN2007667,
 TKIDN2009092, TKIDN2009641, TKIDN2009889, TKIDN2010934,
 15 TKIDN2012824, TKIDN2013287, TKIDN2014757, TKIDN2014771,
 TKIDN2015263, TKIDN2015788, TKIDN2016309, TKIDN2019116,
 TRACH2001443, TRACH2001684, TRACH2007834, TRACH2008300,
 TRACH3001427, UTERU2002410, UTERU2023175, UTERU3001572
 BLADE2006830, BRALZ2017844, CTONG2028758, FCBBF1000509,
 20 FEBRA2001990, FEBRA2028516, HCHON2000508, MESAN2005303,
 NT2RI2009583, TESTI2015626, TKIDN2008778, TKIDN2012771,
 TKIDN2018926

The result of comparative analysis of cDNA libraries
 derived from liver tumor (TLIVE) and normal liver (LIVER) (Table
 25 15) showed that the genes whose expression levels were different
 between the two were 35 and six clones as described below.

BRCAN2018935, BRSTN2016470, BRTHA2012980, BRTHA3002427,
 CTONG2028124, LIVER2007415, NT2RI2008724, SPLEN2012624,
 SPLEN2033098, TESOP2002451, TLIVE2000023, TLIVE2001327,
 30 TLIVE2001828, TLIVE2001927, TLIVE2002336, TLIVE2002338,
 TLIVE2002690, TLIVE2003197, TLIVE2003225, TLIVE2003381,
 TLIVE2003970, TLIVE2004110, TLIVE2004320, TLIVE2004601,
 TLIVE2005180, TLIVE2006236, TLIVE2006529, TLIVE2007132,
 TLIVE2007528, TLIVE2007816, TLIVE2008083, TLIVE2008229,
 35 TLIVE2009541, UTERU2002410, UTERU2005621

LIVER2000247, NT2RI2009583, TESTI2015626, TLIVE2001684,
TLIVE2002046, TLIVE2007607

The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) (Table 16) showed that the genes whose expression levels were different between the two were 47 and nine clones as described below.

5 BRCAN2021028, BRHIP2000819, BRSTN2016470, CTONG1000087,
CTONG2028124, HCHON2006250, HEART1000074, HLUNG1000017,
HLUNG2000014, HLUNG2001996, HLUNG2002465, HLUNG2002958,
10 HLUNG2003003, HLUNG2003872, HLUNG2010464, HLUNG2011041,
HLUNG2011298, HLUNG2012049, HLUNG2012287, HLUNG2012727,
HLUNG2013204, HLUNG2013304, HLUNG2013622, HLUNG2013851,
HLUNG2014262, HLUNG2014288, HLUNG2014449, HLUNG2015617,
HLUNG2017350, HLUNG2017546, HLUNG2017806, HLUNG2019058,
15 HSYRA2008376, KIDNE2012945, NT2RI2003993, NT2RP7013795,
OCBBF3000483, SPLEN2028914, SPLEN2031547, SYNOV4007671,
TESOP1000127, TESTI2003573, TESTI4000014, TESTI4037156,
TRACH2005811, TRACH3004068, UTERU2005621
FEBRA2028516, HCHON2000508, HLUNG2013350, HLUNG2015418,
20 HLUNG2015548, HLUNG2016862, NT2RI2009583, TESTI2015626,
TRACH2019672

The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table 17A) showed the genes whose expression levels were different between the two were 16 clones as described below.

25 CTONG2019788, FEBRA2014213, HLUNG2017546, NOVAR2000136,
NOVAR2000710, NOVAR2000962, NOVAR2001108, NOVAR2001783,
OCBBF3007516, TESTI2052693, TOVAR2000649, TOVAR2001281,
TOVAR2001730, TOVAR2002247, TOVAR2002549, TRACH3004068

30 The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) (Table 17B) showed the gene whose expression levels were different between the two was one clone as described below. The gene has no different expression levels between normal and diseased ovary.
35 However, the gene showed significantly different expression level in both ovary tumor and normal ovary, compared with other

tissues. Thus, the gene are ovary-specific gene and can be used as diagnostic marker because its association with the disease.

TESTI2015626

5 The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) (Table 18) showed that the genes whose expression levels were different between the two were 31 and five clones as described below.

BRACE2024627, BRAWH2014645, BRCAN2028355, BRHIP2000819,
10 BRSTN2016470, BRTHA3003490, COLON2002443, HEART1000010,
HLUNG2002465, KIDNE2001847, NT2RP7000466, PUAEN2006328,
SMINT2001818, STOMA1000189, STOMA2003444, STOMA2004294,
STOMA2004925, STOMA2008546, SYNOV4007671, TESTI4000014,
TESTI4010851, THYMU2035735, TRACH2001549, TRACH2005811,
15 TRACH2025535, TSTOM1000135, TSTOM2000442, TSTOM2000553,
TSTOM2002672, UTERU2006115, UTERU3001572

The following five clones also had different expression levels between the two.

FEBRA2008692, NT2RI2009583, STOMA2003158, STOMA2004893,
20 TESTI2015626

The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) (Table 19) showed that the genes whose expression levels were different between the two were 244 and 34 clones as described
25 below.

BNGH42007788, BRACE1000186, BRACE2030341, BRACE3008772,
BRACE3009747, BRACE3010428, BRACE3027478, BRALZ2017359,
BRAWH2014645, BRAWH3000314, BRAWH3001326, BRAWH3002574,
BRAWH3002821, BRAWH3003727, BRAWH3007592, BRCAN2009432,
30 BRCAN2028355, BRHIP3007586, BRHIP3008344, BRHIP3008565,
BRSSN2006892, BRSTN2001067, BRSTN2016470, BRTHA2010608,
BRTHA3003074, CTONG1000087, CTONG1000467, CTONG2028124,
CTONG3001123, CTONG3008894, CTONG3009028, CTONG3009239,
FCBBF3004847, FEBRA2026984, FEBRA2028618, HCHON2000244,
35 HCHON2000418, HCHON2000626, HCHON2001084, HCHON2001217,
HCHON2005921, HCHON2006250, HCHON2008444, HLUNG2003003,

HSYRA2008376, KIDNE2002252, MESAN2014295, NOVAR2000710,
 NT2RI2008724, NT2RI2014247, NT2RI2014733, NT2RI3002892,
 NT2RI3005724, NT2RI3006284, NT2RI3006340, NT2RI3006673,
 NT2RI3007291, NT2RI3007543, NT2RP7004123, NT2RP7005529,
 5 NT2RP7009147, NT2RP7017474, OCBBF2007028, OCBBF2020741,
 OCBBF2024850, OCBBF2036743, OCBBF3000483, PLACE6001185,
 PLACE7000514, PUAEN2007044, PUAEN2009655, SKNSH2000482,
 SPLEN2006122, SPLEN2016554, SPLEN2031547, SPLEN2036932,
 STOMA1000189, STOMA2004925, SYNOV2017055, SYNOV4001395,
 10 SYNOV4002346, SYNOV4008440, TCERX2000613, TESOP2002273,
 TESTI4000014, TESTI4008797, TESTI4009286, TESTI4012702,
 TESTI4013675, TESTI4014159, TESTI4018886, TESTI4029671,
 TESTI4037156, THYMU2008725, THYMU2031890, THYMU2033070,
 THYMU2035735, THYMU3001472, TRACH1000205, TRACH2001443,
 15 TRACH2001549, TRACH2005811, TRACH2007834, TRACH2008300,
 TRACH3002192, TRACH3003379, TRACH3004068, TRACH3004721,
 TRACH3007479, TUTER1000122, TUTER2000425, TUTER2000904,
 TUTER2000916, TUTER2001387, TUTER2002729, UTERU1000024,
 UTERU1000031, UTERU1000148, UTERU1000249, UTERU1000337,
 20 UTERU1000339, UTERU2000649, UTERU2001409, UTERU2002410,
 UTERU2002841, UTERU2004688, UTERU2004929, UTERU2005004,
 UTERU2005621, UTERU2006115, UTERU2006137, UTERU2006568,
 UTERU2007444, UTERU2007520, UTERU2007724, UTERU2008347,
 UTERU2014678, UTERU2017762, UTERU2019491, UTERU2019681,
 25 UTERU2019706, UTERU2019940, UTERU2020491, UTERU2020718,
 UTERU2021163, UTERU2021380, UTERU2022020, UTERU2022981,
 UTERU2023039, UTERU2023175, UTERU2023651, UTERU2023712,
 UTERU2024002, UTERU2024656, UTERU2025025, UTERU2025645,
 UTERU2025891, UTERU2026025, UTERU2026090, UTERU2026203,
 30 UTERU2027591, UTERU2029953, UTERU2030213, UTERU2030280,
 UTERU2031084, UTERU2031268, UTERU2031521, UTERU2031703,
 UTERU2031851, UTERU2033375, UTERU2033382, UTERU2035114,
 UTERU2035323, UTERU2035328, UTERU2035331, UTERU2035452,
 UTERU2035469, UTERU2035503, UTERU2035745, UTERU2036089,
 35 UTERU2037361, UTERU2037577, UTERU2038251, UTERU3000226,
 UTERU3000645, UTERU3000665, UTERU3000828, UTERU3000899,

UTERU3001059, UTERU3001240, UTERU3001542, UTERU3001571,
 UTERU3001572, UTERU3001585, UTERU3001652, UTERU3001766,
 UTERU3001988, UTERU3002209, UTERU3002218, UTERU3002383,
 UTERU3002667, UTERU3002731, UTERU3002768, UTERU3002786,
 5 UTERU3002993, UTERU3003116, UTERU3003135, UTERU3003178,
 UTERU3003465, UTERU3003523, UTERU3003776, UTERU3004523,
 UTERU3004616, UTERU3004709, UTERU3004992, UTERU3005049,
 UTERU3005205, UTERU3005230, UTERU3005460, UTERU3005585,
 UTERU3005907, UTERU3005970, UTERU3006008, UTERU3006308,
 10 UTERU3007134, UTERU3007419, UTERU3007640, UTERU3007913,
 UTERU3008660, UTERU3008671, UTERU3009259, UTERU3009490,
 UTERU3009517, UTERU3009690, UTERU3009871, UTERU3009979,
 UTERU3011063, UTERU3015086, UTERU3015500, UTERU3016789,
 UTERU3018081, UTERU3018154, UTERU3018616, UTERU3018711
 15 ADRGL2000042, BRHIP3000017, CTONG2003348, CTONG2019822,
 CTONG2020378, CTONG2020411, CTONG2024031, FEBRA2028516,
 HCASM2008536, HCHON2000743, IMR322001879, MESAN2005303,
 NT2RI2009583, OCBBF2008144, PERIC2007068, SPLEN2039379,
 TESTI2015626, TESTI4013894, TUTER2000057, UTERU2004299,
 20 UTERU2008040, UTERU2011220, UTERU2019534, UTERU2021820,
 UTERU2028734, UTERU2032279, UTERU2033577, UTERU2035978,
 UTERU3000402, UTERU3000738, UTERU3001053, UTERU3014791,
 UTERU3015412, UTERU3017176

The result of comparative analysis of cDNA libraries
 25 derived from tongue cancer (CTONG) and normal tongue (NTONG)
 (Table 20) showed that the genes whose expression levels were
 different between the two were 166 and 31 clones as described
 below.

BNGH42007788, BRACE1000186, BRACE2006319, BRACE3010428,
 30 BRACE3012364, BRAMY2020058, BRAMY3002803, BRAWH2001671,
 BRAWH2014645, BRAWH3002574, BRCAN2009432, BRCAN2015371,
 BRCAN2020710, BRHIP2004814, BRHIP3018797, BRTHA2003461,
 BRTHA3003490, CTONG1000087, CTONG1000088, CTONG1000288,
 CTONG1000302, CTONG1000341, CTONG1000467, CTONG1000488,
 35 CTONG1000508, CTONG1000540, CTONG2000042, CTONG2001877,
 CTONG2004062, CTONG2006798, CTONG2008233, CTONG2009423,

CTONG2009531, CTONG2010803, CTONG2013178, CTONG2017500,
 CTONG2019248, CTONG2019652, CTONG2019704, CTONG2019788,
 CTONG2019833, CTONG2020127, CTONG2020522, CTONG2020638,
 CTONG2020806, CTONG2021132, CTONG2022153, CTONG2022601,
 5 CTONG2023021, CTONG2023512, CTONG2024206, CTONG2024749,
 CTONG2025496, CTONG2025516, CTONG2025900, CTONG2026920,
 CTONG2027327, CTONG2028124, CTONG2028687, CTONG3000084,
 CTONG3000657, CTONG3000686, CTONG3000707, CTONG3000896,
 CTONG3001123, CTONG3001370, CTONG3001420, CTONG3001560,
 10 CTONG3002020, CTONG3002127, CTONG3002412, CTONG3002674,
 CTONG3003179, CTONG3003483, CTONG3003652, CTONG3003654,
 CTONG3003737, CTONG3003905, CTONG3003972, CTONG3004072,
 CTONG3004712, CTONG3005325, CTONG3005648, CTONG3005713,
 CTONG3005813, CTONG3006067, CTONG3006186, CTONG3006650,
 15 CTONG3007444, CTONG3007528, CTONG3007586, CTONG3007870,
 CTONG3008252, CTONG3008258, CTONG3008496, CTONG3008566,
 CTONG3008639, CTONG3008831, CTONG3008894, CTONG3008951,
 CTONG3009028, CTONG3009227, CTONG3009239, CTONG3009328,
 CTONG3009385, FEBRA2007544, FEBRA2007801, FEBRA2021966,
 20 FEBRA2025427, HCHON2000028, HCHON2001217, HHDPC1000118,
 HSYRA2008376, KIDNE2001847, KIDNE2002252, MESAN2006563,
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 25 NTONG2005277, NTONG2005969, NTONG2006354, NTONG2007249,
 NTONG2007517, NTONG2008088, NTONG2008672, OCBBF2001794,
 OCBBF2006151, PEBLM2004666, PEBLM2005183, SPLEN2002467,
 SPLEN2029912, SPLEN2031547, SYNOV4007671, SYNOV4008440,
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 30 TESTI4000209, TESTI4008018, TESTI4009286, TESTI4010851,
 TESTI4012702, TESTI4013675, THYMU2031847, THYMU2033308,
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 TRACH3001427, TSTOM2000553, UTERU2005621, UTERU2017762,
 UTERU2023175, UTERU3001572
 35 BLADE2006830, BRHIP3000017, CTONG1000113, CTONG2003348,
 CTONG2004000, CTONG2008721, CTONG2015596, CTONG2015633,

CTONG2016942, CTONG2019822, CTONG2020374, CTONG2020378,
 CTONG2020411, CTONG2020974, CTONG2024031, CTONG2028758,
 CTONG3001501, CTONG3002552, CTONG3003598, CTONG3004550,
 CTONG3004726, CTONG3009287, FEBRA2008692, FEBRA2028516,
 5 HCHON2000508, NT2RI2009583, NTONG2008093, PERIC2007068,
 TESOP2007384, TLIVE2002046, TRACH2000862

These genes are involved in cancer.

Further, there is a method to search for genes involved in
 development and differentiation, which is the expression
 10 frequency analysis in which the expression levels of genes are
 compared between developing and/or differentiating tissues
 and/or cells and adult tissues and/or cells. The genes involved
 in tissue development and/or differentiation are genes
 participating in tissue construction and expression of function,
 15 and thus are useful genes, which are available for regenerative
 medicine aiming at convenient regeneration of injured tissues.

By using the information of gene expression frequency
 gained from the database of nucleotide sequences of 1,402,069
 clones as described above, genes whose expression frequencies
 20 were different between developing and/or differentiating tissues
 and/or cells and adult tissues and/or cells were analyzed.

The result of comparative analysis of cDNA libraries
 derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain
 (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN
 25 or BRTHA) (Table 21) showed that the genes whose expression
 levels were different between the two were 1,035 and 139 clones
 as described below.

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 30 BLADE2004089, BLADE2008398, BNGH42007788, BRACE1000186,
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 BRACE2005457, BRACE2006319, BRACE2008594, BRACE2010489,
 BRACE2011747, BRACE2014306, BRACE2014475, BRACE2014657,
 BRACE2015058, BRACE2015314, BRACE2016981, BRACE2018762,
 35 BRACE2024627, BRACE2026836, BRACE2027258, BRACE2027970,
 BRACE2028970, BRACE2029112, BRACE2029849, BRACE2030326,

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BRACE2031527, BRACE2031531, BRACE2031899, BRACE2032044,
BRACE2032329, BRACE2032385, BRACE2032538, BRACE2032823,
BRACE2033720, BRACE2035381, BRACE2035441, BRACE2036005,
5 BRACE2036096, BRACE2036830, BRACE2036834, BRACE2037847,
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BRACE2039327, BRACE2039475, BRACE2039734, BRACE2040138,
BRACE2040325, BRACE2041009, BRACE2041200, BRACE2041264,
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BRACE3009701, BRACE3009708, BRACE3009724, BRACE3009747,
BRACE3010397, BRACE3010428, BRACE3011271, BRACE3011421,
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UTERU3005230, UTERU3005460, UTERU3005907, UTERU3005970,
UTERU3006308, UTERU3007419, UTERU3007640, UTERU3007913,
UTERU3009259, UTERU3009517, UTERU3009871
35 ADRGL2000042, BLADE2006830, BRACE2002589, BRACE2003609,
BRACE2009318, BRACE2011677, BRACE2029396, BRACE2037299,

BRACE2039823, BRACE2039832, BRACE2043105, BRACE3001058,
 BRACE3001113, BRACE3003026, BRACE3003053, BRACE3009127,
 BRACE3010076, BRACE3015829, BRACE3021148, BRALZ2017844,
 BRAMY2019111, BRAMY2035070, BRAMY2035449, BRAMY2035718,
 5 BRAMY2038516, BRAMY2039341, BRAMY2040159, BRAMY2041434,
 BRAMY2045471, BRAMY3004800, BRAWH1000369, BRAWH2006207,
 BRAWH2006395, BRAWH2008993, BRAWH2009393, BRAWH2010552,
 BRAWH3007441, BRAWH3009017, BRCAN2002473, BRCAN2002854,
 BRCAN2003070, BRCAN2014229, BRCOC2019841, BRHIP2002722,
 10 BRHIP2003272, BRHIP2005271, BRHIP2005724, BRHIP2006617,
 BRHIP2008389, BRHIP2012360, BRHIP2017553, BRHIP2026877,
 BRHIP3000017, BRHIP3000240, BRHIP3008314, BRHIP3026052,
 BRSTN2013354, BRTHA2002133, BRTHA2002702, BRTHA2007060,
 BRTHA2010033, BRTHA2011321, BRTHA2013426, BRTHA2013610,
 15 BRTHA2016318, BRTHA2017364, BRTHA2017972, BRTHA2018011,
 BRTHA2018443, BRTHA3000296, BRTHA3003000, BRTHA3008826,
 CTONG2008721, CTONG2020374, CTONG2020378, CTONG2020411,
 CTONG2024031, CTONG3004726, FCBBF1000509, FCBBF3010361,
 FCBBF3027854, FEBRA2000790, FEBRA2001990, FEBRA2006519,
 20 FEBRA2008692, FEBRA2014122, FEBRA2027609, FEBRA2028516,
 HCASM2003018, HCHON2000508, HCHON2000743, HCHON2004858,
 HSYRA2005628, IMR322001879, NT2RI2009583, NT2RP8000521,
 OCBBF2003327, OCBBF2005433, OCBBF2006987, OCBBF2008144,
 OCBBF2009583, OCBBF2011669, OCBBF2019684, OCBBF2020048,
 25 OCBBF2030116, OCBBF2032274, OCBBF2034637, OCBBF3002654,
 OCBBF3003761, OCBBF3004972, PERIC2007068, PUAEN2006335,
 SPLEN2016932, SPLEN2039379, SYNOV2006620, SYNOV2021953,
 TESTI1000266, TESTI2015626, TESTI2026647, TESTI4000214,
 TESTI4001984, TESTI4008058, TESTI4013894, TESTI4015442,
 30 TESTI4017714, TESTI4025268, TESTI4025547, TESTI4026207,
 TESTI4032090, THYMU2004284, THYMU2040925, THYMU3000360,
 TKIDN2018926, TLIVE2002046, TRACH3000134, UTERU2008040,
 UTERU2011220, UTERU2021820, UTERU2028734

The result of comparative analysis of cDNA libraries
 35 derived from fetal heart (FEHRT) and adult heart (HEART) (Table

22) showed that the genes whose expression levels were different between the two were 34 and two clones as described below.

BRAMY2040592, BRAWH2001671, BRSTN2016470, CTONG2017500,
CTONG2028124, CTONG3000657, D3OST3000169, FEBRA2008287,
5 HCHON2000244, HCHON2000626, HEART1000010, HEART1000074,
HEART1000088, HEART1000139, HEART2001680, HEART2001756,
HEART2006131, HEART2006909, HEART2007031, HEART2010391,
HEART2010492, HEART2010495, KIDNE2000665, NB9N41000340,
NT2RI2003993, NT2RI3002892, OCBBF2024850, SKMUS2006394,
10 SMINT2001818, TESTI4000209, TKIDN2015788, TRACH3002192,
TRACH3005294, TRACH3007479
HEART2009680, THYMU2004284

The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE)
15 (Table 23) showed that the genes whose expression levels were different between the two were 40 and two clones as described below.

BRACE2043665, BRACE3010428, BRSTN2016470, CTONG1000087,
CTONG2028124, CTONG3008894, HCASM2003415, HCHON2000244,
20 HEART1000074, HHDPC1000118, KIDNE1000064, KIDNE2000665,
KIDNE2000722, KIDNE2000832, KIDNE2000846, KIDNE2001361,
KIDNE2001847, KIDNE2002252, KIDNE2002991, KIDNE2003837,
KIDNE2005543, KIDNE2006580, KIDNE2010264, KIDNE2011314,
KIDNE2011532, KIDNE2011635, KIDNE2012945, KIDNE2013095,
25 PEBLM2004666, PLACE6019385, STOMA1000189, SYNOV4007671,
TBAES2001258, TESOP2002451, TESTI4000014, TESTI4012702,
THYMU2032014, TRACH2001684, TRACH2007834, UTERU2023175
NT2RI2009583, OCBBF2008144

The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) (Table
30 24) showed that the genes whose expression levels were different between the two were 51 and eight clones as described below.

BRAWH3007592, BRCAN2021028, BRHIP2000819, BRSTN2016470,
CTONG1000087, CTONG2028124, HCASM2007047, HEART1000074,
35 HLUNG1000017, HLUNG2000014, HLUNG2001996, HLUNG2002465,
HLUNG2002958, HLUNG2003003, HLUNG2003872, HLUNG2010464,

HLUNG2011041, HLUNG2011298, HLUNG2012049, HLUNG2012287,
 HLUNG2012727, HLUNG2013204, HLUNG2013304, HLUNG2013622,
 HLUNG2013851, HLUNG2014262, HLUNG2014288, HLUNG2014449,
 HLUNG2015617, HLUNG2017350, HLUNG2017546, HLUNG2017806,
 5 HLUNG2019058, HSYRA2008376, KIDNE2012945, NT2RI2003993,
 NT2RI3007543, OCBBF3000483, SMINT1000192, SPLEN2028914,
 SPLEN2031547, STOMA1000189, SYNOV4007671, TESOP1000127,
 TESTI2003573, TESTI4000014, TESTI4037156, TRACH2005811,
 TRACH3004068, UTERU2005621, UTERU2023175
 10 FEBRA2028516, HCHON2000508, HLUNG2013350, HLUNG2015418,
 HLUNG2015548, HLUNG2016862, TESTI2015626, TRACH2019672

These genes are involved in regeneration of tissues and/or cells.

A nucleotide sequence information-based analysis was
 15 carried out to identify the genes whose expression frequencies
 are higher or lower in CD34+ cell (cell expressing a
 glycoprotein CD34) treated with the osteoclast differentiation
 factor (Molecular Medicine 38. 642-648. (2001)) than in the
 untreated CD34+ cell, which is the precursor cell of
 20 monocyte/macrophage line. The result of comparative analysis
 for the frequency between the two cDNA libraries prepared from
 the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells
 treated with the osteoclast differentiation factor (D30ST, D60ST
 or D90ST) showed following genes whose expression levels were
 25 different between the two.

Table 2

Clone ID	CD34C	D30ST	D60ST	D90ST
BRACE3013780	0.000	55.996	0.000	0.000
BRAMY2047420	42.545	0.000	0.000	0.000
BRSTN2016470	0.000	2.555	0.000	0.000
CTONG3008894	0.000	8.487	0.000	0.000
35 D30ST2002182	0.000	86.773	0.000	0.000
D30ST2002648	0.000	17.515	0.000	0.000

	D30ST3000169	20.553	28.566	0.000	19.796
	PEBLM2005183	0.000	0.000	0.000	50.747
	PUAEN2009655	0.000	0.000	0.000	49.285
	TESTI4000014	7.500	0.000	0.000	0.000
5	TESTI4010851	0.000	0.000	0.000	7.372
	TRACH2023299	0.000	74.521	0.000	0.000
	TRACH2025535	0.000	6.778	0.000	0.000
	TRACH3001427	0.000	0.000	0.000	12.519
	UTERU2006137	0.000	90.731	0.000	0.000
10	HCHON2000508	0.000	4.360	50.138	0.000
	TESTI2015626	0.000	0.000	0.000	4.435

A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed following genes whose expression levels were different between the two.

Table 3

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
BNGH42007788	0.000	7.419	0.000	0.000
BRACE1000186	0.000	5.211	0.000	7.836
BRACE2006319	0.000	8.450	0.000	0.000
BRACE2014306	0.000	0.000	0.000	17.640
BRACE2015058	0.000	10.567	0.000	0.000
BRACE2044286	0.000	0.000	33.923	0.000
BRACE3010428	0.000	0.000	2.080	0.000
BRAMY2044078	0.000	10.567	0.000	0.000
BRAWH2014645	0.000	7.643	1.921	0.000
BRAWH2014662	0.000	0.000	0.000	56.250

	BRAWH3002574	0.000	0.000	12.014	0.000
	BRAWH3003992	0.000	34.956	0.000	0.000
	BRAWH3005981	0.000	70.676	0.000	0.000
	BRAWH3007592	0.000	8.644	3.259	0.000
5	BRCAN2009432	0.000	3.173	0.000	0.000
	BRCAN2016619	0.000	0.000	23.940	0.000
	BRCAN2028355	0.000	0.000	0.000	5.354
	BRHIP2001074	0.000	47.218	0.000	0.000
	BRHIP2007741	0.000	0.000	6.309	6.291
10	BRHIP2014228	0.000	35.475	0.000	0.000
	BRHIP2024146	0.000	0.000	1.106	0.000
	BRHIP3007586	0.000	0.000	0.000	12.507
	BRHIP3018797	0.000	0.000	4.869	0.000
	BRTHA2003461	0.000	0.000	3.989	0.000
15	BRTHA3000633	0.000	0.000	62.102	0.000
	BRTHA3003490	0.000	3.913	0.000	0.000
	COLON2001721	0.000	0.000	10.053	0.000
	CTONG1000087	0.000	5.041	5.701	3.790
	CTONG2008233	0.000	8.275	2.496	7.466
20	CTONG2020638	0.000	0.000	22.499	0.000
	CTONG2028124	0.000	1.211	0.913	0.000
	CTONG3003905	0.000	47.197	0.000	0.000
	CTONG3008894	0.000	7.008	9.247	2.634
	CTONG3009028	0.000	0.000	2.924	0.000
25	CTONG3009239	0.000	0.000	2.624	0.000
	DFNES2011499	0.000	0.000	22.548	0.000
	FCBBF3001977	0.000	17.952	13.536	0.000
	FEBRA1000030	0.000	0.000	0.000	59.247
	FEBRA2006396	0.000	0.000	14.606	0.000
30	FEBRA2007801	0.000	5.950	0.000	0.000
	HCHON2000028	0.000	0.000	5.766	0.000
	HCHON2000244	0.000	3.171	1.195	0.000
	HCHON2001084	0.000	0.000	4.173	0.000
	HCHON2001217	0.000	2.509	5.674	0.000
35	HCHON2001548	0.000	27.583	0.000	0.000
	HCHON2006250	0.000	3.771	0.000	0.000

	HEART1000074	0.000	1.830	0.000	0.000
	HHDPG1000118	0.000	10.102	3.809	15.191
	HSYRA2009075	0.000	2.899	0.000	0.000
	IMR322000127	0.000	3.733	0.000	0.000
5	IMR322001380	0.000	0.000	3.602	7.184
	KIDNE2000665	0.000	0.000	0.000	7.016
	KIDNE2002252	0.000	0.000	3.961	0.000
	MESAN2006563	0.000	1.664	2.510	0.000
	MESAN2012054	0.000	0.000	4.636	0.000
10	MESAN2015515	0.000	6.402	0.000	0.000
	NT2NE2003252	0.000	0.000	0.000	100.000
	NT2NE2005890	0.000	0.000	0.000	64.265
	NT2NE2006531	0.000	0.000	0.000	100.000
	NT2NE2006909	0.000	0.000	0.000	1.034
15	NT2NE2008060	0.000	0.000	0.000	74.472
	NT2RI2003993	0.000	0.000	6.899	0.000
	NT2RI2004618	0.000	0.000	100.000	0.000
	NT2RI2005166	0.000	0.000	47.393	0.000
	NT2RI2006686	0.000	0.000	21.246	0.000
20	NT2RI2008724	0.000	0.000	3.337	0.000
	NT2RI2009855	0.000	0.000	100.000	0.000
	NT2RI2011422	0.000	0.000	100.000	0.000
	NT2RI2011683	0.000	0.000	100.000	0.000
	NT2RI2012659	0.000	0.000	24.645	0.000
25	NT2RI2012990	0.000	0.000	24.360	0.000
	NT2RI2013357	0.000	0.000	73.545	0.000
	NT2RI2014247	0.000	0.000	27.718	0.000
	NT2RI2014551	0.000	0.000	100.000	0.000
	NT2RI2014733	0.000	0.000	45.319	0.000
30	NT2RI2016128	0.000	0.000	100.000	0.000
	NT2RI2018311	0.000	0.000	78.082	0.000
	NT2RI2018883	0.000	0.000	49.384	0.000
	NT2RI2019751	0.000	0.000	71.913	0.000
	NT2RI2023303	0.000	0.000	100.000	0.000
35	NT2RI2025909	0.000	0.000	100.000	0.000
	NT2RI2025957	0.000	0.000	100.000	0.000

	NT2R12027081	0.000	0.000	100.000	0.000
	NT2R12027396	0.000	0.000	100.000	0.000
	NT2R13000622	0.000	0.000	15.558	0.000
	NT2R13001263	0.000	0.000	100.000	0.000
5	NT2R13001515	0.000	0.000	19.682	0.000
	NT2R13002303	0.000	0.000	100.000	0.000
	NT2R13002842	0.000	45.164	34.054	0.000
	NT2R13002892	0.000	4.241	3.198	0.000
	NT2R13003031	0.000	0.000	100.000	0.000
10	NT2R13003095	0.000	0.000	100.000	0.000
	NT2R13003162	0.000	0.000	100.000	0.000
	NT2R13003382	0.000	0.000	71.913	0.000
	NT2R13003409	0.000	0.000	100.000	0.000
	NT2R13004381	0.000	0.000	100.000	0.000
15	NT2R13004510	0.000	0.000	51.230	0.000
	NT2R13005202	0.000	0.000	100.000	0.000
	NT2R13005403	0.000	0.000	62.102	0.000
	NT2R13005724	0.000	14.284	10.770	0.000
	NT2R13006132	0.000	0.000	100.000	0.000
20	NT2R13006171	0.000	0.000	100.000	0.000
	NT2R13006284	0.000	0.000	3.760	0.000
	NT2R13006340	0.000	0.000	14.839	0.000
	NT2R13006376	0.000	0.000	100.000	0.000
	NT2R13006673	0.000	0.000	18.135	0.000
25	NT2R13006796	0.000	0.000	100.000	0.000
	NT2R13007065	0.000	0.000	100.000	0.000
	NT2R13007158	0.000	0.000	100.000	0.000
	NT2R13007291	0.000	0.000	22.746	0.000
	NT2R13007543	0.000	0.000	1.542	6.150
30	NT2R13007757	0.000	30.480	45.964	0.000
	NT2R13007978	0.000	0.000	100.000	0.000
	NT2R13008055	0.000	0.000	40.142	0.000
	NT2R13008162	0.000	0.000	100.000	0.000
	NT2R13008652	0.000	0.000	100.000	0.000
35	NT2R13008697	0.000	0.000	100.000	0.000
	NT2R13008974	0.000	0.000	100.000	0.000

	NT2R13009158	0.000	0.000	45.727	0.000
	NT2RP7000359	0.000	100.000	0.000	0.000
	NT2RP7000466	0.000	2.098	3.164	0.000
	NT2RP7004027	0.000	100.000	0.000	0.000
5	NT2RP7004123	0.000	4.625	0.000	0.000
	NT2RP7005118	0.000	100.000	0.000	0.000
	NT2RP7005529	0.000	35.588	0.000	0.000
	NT2RP7005846	0.000	100.000	0.000	0.000
	NT2RP7009030	0.000	46.373	0.000	0.000
10	NT2RP7009147	0.000	7.679	2.895	0.000
	NT2RP7009867	0.000	100.000	0.000	0.000
	NT2RP7010128	0.000	100.000	0.000	0.000
	NT2RP7010599	0.000	77.250	0.000	0.000
	NT2RP7011570	0.000	100.000	0.000	0.000
15	NT2RP7013795	0.000	10.432	0.000	0.000
	NT2RP7014005	0.000	14.022	21.145	0.000
	NT2RP7015512	0.000	31.156	0.000	0.000
	NT2RP7017365	0.000	100.000	0.000	0.000
	NT2RP7017474	0.000	45.366	0.000	0.000
20	NT2RP7017546	0.000	100.000	0.000	0.000
	NT2RP8000137	0.000	100.000	0.000	0.000
	NT2RP8000296	0.000	100.000	0.000	0.000
	NT2RP8000483	0.000	100.000	0.000	0.000
	NTONG2005969	0.000	15.484	0.000	0.000
25	OCBBF2007028	0.000	0.000	2.509	0.000
	OCBBF2037068	0.000	0.000	27.189	54.224
	PLACE7000514	0.000	0.000	8.644	0.000
	PUAEN2007044	0.000	3.455	13.024	0.000
	SPLEN2002467	0.000	7.852	0.000	0.000
30	SPLEN2006122	0.000	0.000	1.530	0.000
	SPLEN2028914	0.000	6.730	10.149	0.000
	SPLEN2031547	0.000	0.000	2.861	0.000
	SYNOV4002346	0.000	0.000	10.899	0.000
	SYNOV4007671	42.189	0.000	0.000	2.657
35	SYNOV4008440	0.000	0.000	2.681	0.000
	TESOP2002273	0.000	9.782	0.000	0.000

	TESTI2003573	0.000	0.000	13.573	0.000
	TESTI4000014	0.000	3.443	0.974	0.000
	TESTI4009286	0.000	1.747	0.000	0.000
	TESTI4010851	0.000	5.270	1.987	0.000
5	TESTI4012702	0.000	0.000	3.961	0.000
	TESTI4029671	0.000	44.826	0.000	0.000
	TESTI4037156	0.000	4.669	1.509	2.006
	THYMU3000133	0.000	34.767	8.738	0.000
	TRACH1000205	0.000	0.000	7.152	0.000
10	TRACH2005811	0.000	0.000	0.000	3.822
	TRACH2007834	0.000	3.647	1.833	0.000
	TRACH2025535	0.000	1.399	3.165	4.208
	TRACH3001427	0.000	8.951	1.687	3.365
	TRACH3002192	0.000	0.000	2.267	4.520
15	TRACH3004721	0.000	14.013	5.283	10.536
	TRACH3008093	0.000	0.000	8.902	0.000
	TRACH3008535	0.000	68.270	0.000	0.000
	TRACH3008713	0.000	68.270	0.000	0.000
	UTERU2002410	0.000	0.000	1.067	0.000
20	UTERU2023175	0.000	7.176	0.000	5.396
	ADRL2000042	0.000	0.000	0.000	9.204
	BRACE2003609	0.000	21.907	0.000	32.942
	BRACE3003026	0.000	0.000	59.349	0.000
	BRHIP3000017	0.000	0.000	8.013	0.000
25	CTONG2020411	0.000	16.593	25.022	0.000
	FCBBF1000509	0.000	0.000	0.000	6.762
	FCBBF3027854	0.000	0.000	28.447	0.000
	FEBRA2028516	0.000	11.027	6.236	0.000
	HCHON2000508	0.000	0.900	0.000	0.000
30	IMR322001879	0.000	0.000	35.028	0.000
	NT2RI2005772	0.000	0.000	100.000	0.000
	NT2RI2008952	0.000	0.000	100.000	0.000
	NT2RI2009583	0.000	0.000	0.813	0.811
	NT2RI2018448	0.000	15.176	11.442	0.000
35	NT2RI2027157	0.000	0.000	100.000	0.000
	NT2RI3000174	0.000	0.000	61.866	0.000

	NT2RI3001132	0.000	0.000	100.000	0.000
	NT2RI3002557	0.000	0.000	100.000	0.000
	NT2RI3005928	0.000	0.000	100.000	0.000
	NT2RI3007167	0.000	0.000	100.000	0.000
5	NT2RI3007443	0.000	0.000	100.000	0.000
	NT2RP7008435	0.000	100.000	0.000	0.000
	NT2RP8000521	0.000	62.933	0.000	0.000
	OCBBF2006987	0.000	62.306	0.000	0.000
	PERIC2007068	0.000	3.719	2.804	0.000
10	TESTI2015626	9.463	0.000	0.000	2.384
	TESTI4015442	0.000	48.593	0.000	0.000
	TLIVE2002046	0.000	0.000	3.298	0.000
	TRACH3000134	0.000	43.581	0.000	0.000
	TUTER2000057	0.000	0.000	7.539	0.000

15

The result of comparative analysis of cDNA libraries derived from the cerebral cortex of Alzheimer patients (BRALZ and BRASW), and from whole tissues of a normal brain (BRAWH) showed the following genes whose expression levels differed between the two.

20

Table 4

Clone ID	BRAWH	BRALZ	BRASW
25			
	ASTR01000009	2.611	0.000
	BLADE2008398	12.401	0.000
	BRACE1000186	4.324	0.000
	BRACE1000258	31.956	0.000
30	BRACE1000533	11.795	0.000
	BRACE2005457	58.488	0.000
	BRACE2010489	63.510	0.000
	BRACE2014657	15.451	0.000
	BRACE2035381	10.177	0.000
35	BRACE2044286	18.667	0.000
	BRACE2045954	27.309	0.000

	BRACE3000787	32.844	0.000	0.000
	BRACE3003192	58.488	0.000	0.000
	BRACE3005499	31.276	0.000	0.000
	BRACE3007480	19.471	0.000	0.000
5	BRACE3009237	18.139	0.000	0.000
	BRACE3009724	58.488	0.000	0.000
	BRACE3009747	2.237	0.000	0.000
	BRACE3010428	6.868	0.000	0.000
	BRACE3011271	11.036	0.000	0.000
10	BRACE3011421	28.251	0.000	0.000
	BRACE3012364	8.506	0.000	0.000
	BRACE3022769	4.285	0.000	0.000
	BRACE3026735	24.173	0.000	0.000
	BRACE3031838	58.488	0.000	0.000
15	BRALZ2011796	5.511	39.830	0.000
	BRALZ2012183	0.000	100.000	0.000
	BRALZ2012848	0.000	100.000	0.000
	BRALZ2014484	0.000	100.000	0.000
	BRALZ2016085	0.000	100.000	0.000
20	BRALZ2016498	0.000	100.000	0.000
	BRALZ2017359	0.000	75.184	0.000
	BRAMY2003008	26.445	0.000	0.000
	BRAMY2005052	11.612	0.000	0.000
	BRAMY2019300	49.811	0.000	0.000
25	BRAMY2019963	20.428	0.000	0.000
	BRAMY2036567	7.474	0.000	0.000
	BRAMY2037823	29.664	0.000	0.000
	BRAMY2040592	3.482	12.582	0.000
	BRAMY3002803	14.428	0.000	0.000
30	BRAMY3004224	33.027	0.000	0.000
	BRAMY3005091	19.193	0.000	0.000
	BRASW1000053	0.000	0.000	100.000
	BRASW1000125	0.000	0.000	99.054
	BRAWH1000127	15.983	0.000	0.000
35	BRAWH2001395	14.290	3.037	0.000
	BRAWH2001671	7.605	0.000	0.000

	BRAWH2001940	37.398	0.000	0.000
	BRAWH2001973	37.398	0.000	0.000
	BRAWH2002560	6.454	0.000	0.000
	BRAWH2002761	100.000	0.000	0.000
5	BRAWH2005315	100.000	0.000	0.000
	BRAWH2007658	58.101	0.000	0.000
	BRAWH2010000	18.745	0.000	0.000
	BRAWH2010084	100.000	0.000	0.000
	BRAWH2010536	14.718	0.000	0.000
10	BRAWH2012162	36.060	0.000	0.000
	BRAWH2012326	100.000	0.000	0.000
	BRAWH2013294	39.442	0.000	0.000
	BRAWH2013871	37.485	0.000	0.000
	BRAWH2014414	17.865	0.000	0.000
15	BRAWH2014645	4.228	0.000	0.000
	BRAWH2014662	15.521	0.000	0.000
	BRAWH2014876	10.473	0.000	0.000
	BRAWH2014954	58.488	0.000	0.000
	BRAWH2016221	47.417	0.000	0.000
20	BRAWH2016439	100.000	0.000	0.000
	BRAWH2016702	73.807	0.000	0.000
	BRAWH2016724	35.119	0.000	0.000
	BRAWH3000078	100.000	0.000	0.000
	BRAWH3000100	100.000	0.000	0.000
25	BRAWH3000314	71.553	0.000	0.000
	BRAWH3000491	100.000	0.000	0.000
	BRAWH3001326	45.606	0.000	0.000
	BRAWH3001475	100.000	0.000	0.000
	BRAWH3001891	34.539	0.000	0.000
30	BRAWH3002574	13.222	0.000	0.000
	BRAWH3002600	36.800	0.000	0.000
	BRAWH3002819	100.000	0.000	0.000
	BRAWH3002821	21.953	0.000	0.000
	BRAWH3003522	100.000	0.000	0.000
35	BRAWH3003555	15.229	0.000	0.000
	BRAWH3003727	10.055	0.000	0.000

	BRAWH3003801	100.000	0.000	0.000
	BRAWH3003992	29.008	0.000	0.000
	BRAWH3004453	100.000	0.000	0.000
	BRAWH3004666	49.499	0.000	0.000
5	BRAWH3005132	49.811	0.000	0.000
	BRAWH3005422	100.000	0.000	0.000
	BRAWH3005912	100.000	0.000	0.000
	BRAWH3005981	29.324	0.000	0.000
	BRAWH3006548	71.018	0.000	0.000
10	BRAWH3006792	49.499	0.000	0.000
	BRAWH3007221	100.000	0.000	0.000
	BRAWH3007506	100.000	0.000	0.000
	BRAWH3007592	8.966	0.000	0.000
	BRAWH3007726	54.530	0.000	0.000
15	BRAWH3007783	100.000	0.000	0.000
	BRAWH3008341	100.000	0.000	0.000
	BRAWH3008697	100.000	0.000	0.000
	BRAWH3008931	3.463	0.000	0.000
	BRAWH3009297	58.488	0.000	0.000
20	BRC0C2003213	10.381	0.000	0.000
	BRC0C2014033	15.633	0.000	0.000
	BRC0C2020142	22.014	0.000	0.000
	BRHIP2000920	36.630	0.000	0.000
	BRHIP2005719	49.499	0.000	0.000
25	BRHIP2007741	6.943	0.000	0.000
	BRHIP2014228	29.439	0.000	0.000
	BRHIP2024146	3.042	12.091	0.000
	BRHIP2026288	0.000	77.982	0.000
	BRHIP3000339	14.290	3.037	0.000
30	BRHIP3006683	24.100	0.000	0.000
	BRHIP3007586	17.255	0.000	0.000
	BRHIP3008405	35.187	0.000	0.000
	BRHIP3018797	30.810	4.840	0.000
	BRSSN2000684	23.433	0.000	0.000
35	BRSSN2011738	31.553	0.000	0.000
	BRSSN2014299	3.695	0.000	0.000

	BRSTN2008052	32.844	0.000	0.000
	BRSTN2015015	14.017	0.000	0.000
	BRSTN2016470	0.438	7.909	0.000
	BRTHA1000311	11.803	0.000	0.000
5	BRTHA2008335	16.281	0.000	0.000
	BRTHA3002427	8.577	0.000	0.000
	BRTHA3003490	1.623	0.000	0.000
	BRTHA3008520	47.417	0.000	0.000
	BRTHA3017848	47.417	0.000	0.000
10	COLON2001721	11.065	0.000	0.000
	CTONG2017500	2.649	0.000	0.000
	CTONG2028124	0.503	0.000	0.000
	CTONG3000657	3.880	0.000	0.000
	CTONG3001123	7.847	0.000	0.000
15	CTONG3009328	11.993	43.334	0.000
	FCBBF2001183	16.537	5.975	0.000
	FCBBF3001977	7.448	0.000	0.000
	FEBRA2007544	14.689	0.000	0.000
	FEBRA2007801	4.937	0.000	0.000
20	FEBRA2020886	12.124	0.000	0.000
	FEBRA2028618	5.082	0.000	0.000
	HCASM2007047	3.431	0.000	0.000
	HCHON2000244	0.658	0.000	0.000
	HCHON2000626	2.351	0.000	0.000
25	HCHON2001217	3.123	0.000	0.000
	HCHON2002676	13.647	0.000	0.000
	HCHON2006250	1.565	0.000	0.000
	HEART1000074	0.759	0.000	0.000
	HHDPC1000118	2.096	0.000	0.000
30	HLUNG2002465	1.209	0.000	0.000
	IMR322000127	3.098	5.597	0.000
	IMR322001380	0.000	7.163	0.000
	IMR322002035	36.176	0.000	0.000
	KIDNE2006580	7.013	0.000	0.000
35	MESAN2006563	0.691	0.000	0.000
	MESAN2012054	12.754	0.000	0.000

	MESTC1000042	2.245	0.000	0.000
	NOVAR2001783	4.027	0.000	0.000
	NT2NE2006909	0.285	0.000	0.000
	NT2RI2008724	1.836	0.000	0.000
5	NT2RI2012659	13.562	0.000	0.000
	NT2RI2014733	24.938	0.000	0.000
	NT2RI3002892	8.799	0.000	0.000
	NT2RI3006284	4.138	0.000	0.000
	NT2RI3006673	19.959	0.000	0.000
10	NT2RI3007543	1.697	0.000	0.000
	NT2RI3008055	44.179	0.000	0.000
	NT2RP7005529	14.766	0.000	0.000
	NT2RP7009147	14.337	0.000	0.000
	NT2RP7014005	5.818	0.000	0.000
15	NT2RP7017474	18.823	0.000	0.000
	NTONG2005969	0.000	11.607	0.000
	OCBBF2001794	4.728	0.000	0.000
	OCBBF2006005	9.535	0.000	0.000
	OCBBF2006764	15.345	0.000	0.000
20	OCBBF2007028	9.665	0.000	0.000
	OCBBF2007114	0.000	38.623	0.000
	OCBBF2010140	32.508	0.000	0.000
	OCBBF2021286	18.456	0.000	0.000
	OCBBF2023162	0.000	37.152	0.000
25	OCBBF2024850	4.445	0.000	0.000
	OCBBF2028935	5.789	4.183	0.000
	OCBBF2036743	11.053	0.000	0.000
	OCBBF2038317	19.713	0.000	0.000
	OCBBF3000483	11.973	0.000	0.000
30	OCBBF3008230	29.840	0.000	0.000
	PEBLM2004666	3.715	0.000	0.000
	PLACE6001185	21.358	0.000	0.000
	PUAEN2005930	18.362	0.000	0.000
	PUAEN2006701	2.249	8.128	0.000
35	PUAEN2007044	8.600	0.000	0.000
	PUAEN2009655	18.275	0.000	0.000

	SMINT2001818	0.000	3.387	0.000
	SPLEN2028914	2.792	0.000	0.000
	SPLEN2031424	15.229	0.000	0.000
	SPLEN2031547	1.574	5.689	0.000
5	SPLEN2034781	27.984	0.000	0.000
	SPLEN2036932	2.932	0.000	0.000
	SYNOV2014400	12.977	0.000	0.000
	SYNOV4002346	5.997	0.000	0.000
	SYNOV4002883	23.940	0.000	0.000
10	SYNOV4007430	31.677	0.000	0.000
	SYNOV4007671	0.000	2.649	0.000
	SYNOV4008440	1.475	0.000	0.000
	TESOP2002273	0.000	14.666	0.000
	TESOP2002451	2.375	0.000	0.000
15	TESTI4000014	1.964	0.000	0.000
	TESTI4000209	2.649	0.000	0.000
	TESTI4001100	4.098	0.000	0.000
	TESTI4006137	25.755	0.000	0.000
	TESTI4008797	12.429	0.000	0.000
20	TESTI4009286	1.450	0.000	0.000
	TESTI4010851	3.280	0.000	0.000
	TESTI4013817	27.163	0.000	0.000
	TESTI4014694	2.229	0.000	0.000
	TESTI4021478	22.098	0.000	0.000
25	TESTI4022936	26.445	0.000	0.000
	TESTI4024420	37.398	0.000	0.000
	TESTI4027821	60.471	0.000	0.000
	THYMU2001090	21.252	0.000	0.000
	THYMU2033308	13.964	0.000	0.000
30	THYMU2035735	1.319	0.000	0.000
	THYMU2039315	54.530	0.000	0.000
	THYMU3001234	11.085	0.000	0.000
	THYMU3008171	20.170	0.000	0.000
	TKIDN2009641	5.782	0.000	0.000
35	TKIDN2009889	35.077	0.000	0.000
	TKIDN2015788	5.261	9.505	0.000

	TRACH1000205	19.677	0.000	0.000
	TRACH2001549	8.457	0.000	0.000
	TRACH2005811	2.109	0.000	0.000
	TRACH2006049	47.167	0.000	0.000
5	TRACH2007834	0.504	0.000	0.000
	TRACH2008300	10.186	6.135	0.000
	TRACH2025535	5.806	0.000	0.000
	TRACH3001427	5.571	3.355	0.000
	TRACH3002192	4.989	2.253	0.000
10	TRACH3004068	0.000	5.150	0.000
	TRACH3004721	8.721	0.000	0.000
	TRACH3005294	7.428	0.000	0.000
	TRACH3007479	1.075	0.000	0.000
	TRACH3008093	2.449	0.000	0.000
15	TRACH3009455	47.167	0.000	0.000
	UTERU2005621	0.000	8.145	0.000
	UTERU2006115	7.837	0.000	0.000
	UTERU2019706	45.606	0.000	0.000
	UTERU2023039	45.606	0.000	0.000
20	UTERU2026203	45.606	0.000	0.000
	UTERU3005230	24.419	0.000	0.000
	UTERU3007640	45.606	0.000	0.000
	UTERU3009871	36.230	0.000	0.000
	ADRGL2000042	2.540	0.000	0.000
25	BLADE2006830	1.681	0.000	0.000
	BRACE2003609	9.090	0.000	0.000
	BRALZ2017844	0.000	49.396	0.000
	BRAMY3004800	38.061	0.000	0.000
	BRAWH1000369	100.000	0.000	0.000
30	BRAWH2006207	12.943	0.000	0.000
	BRAWH2006395	12.446	0.000	0.000
	BRAWH2008993	49.811	0.000	0.000
	BRAWH2009393	100.000	0.000	0.000
	BRAWH2010552	58.488	0.000	0.000
35	BRAWH3007441	100.000	0.000	0.000
	BRAWH3009017	100.000	0.000	0.000

	BRHIP2005271	7.083	0.000	0.000
	BRHIP3000017	8.819	0.000	0.000
	BRHIP3026052	0.000	54.140	0.000
	BRTHA2018443	22.098	0.000	0.000
5	BRTHA3003000	17.150	0.000	0.000
	CTONG2020374	31.081	0.000	0.000
	CTONG2020378	16.140	0.000	0.000
	CTONG2024031	2.584	0.000	0.000
	FCBBF1000509	3.732	0.000	0.000
10	FEBRA2001990	18.144	0.000	0.000
	FEBRA2006519	11.891	0.000	0.000
	FEBRA2028516	8.007	0.000	0.000
	HCHON2000743	6.105	0.000	0.000
	IMR322001879	9.638	0.000	0.000
15	NT2R12009583	0.224	0.808	0.000
	OCBBF2008144	5.768	0.000	0.000
	PERIC2007068	3.086	0.000	0.000
	PUAEN2006335	12.682	0.000	0.000
	SPLEN2039379	5.792	0.000	0.000
20	TEST14001984	60.471	0.000	0.000
	TEST14008058	8.814	0.000	0.000
	TEST14025268	60.471	0.000	0.000
	TEST14032090	60.471	0.000	0.000
	THYMU3000360	39.314	0.000	0.000
25	TLIVE2002046	5.445	0.000	0.000
	TRACH3000134	36.165	0.000	0.000
	UTERU2021820	24.929	0.000	0.000
	UTERU2028734	21.953	0.000	0.000

30 The result of comparative analysis of cDNA libraries derived from the substantia nigra (BRSSN), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

35 Table 5

	Clone ID	BRAWH	BRSSN
	ASTR01000009	2.611	0.000
	BLADE2008398	12.401	0.000
5	BRACE1000186	4.324	0.000
	BRACE1000258	31.956	0.000
	BRACE1000533	11.795	8.780
	BRACE2005457	58.488	0.000
	BRACE2010489	63.510	0.000
10	BRACE2014657	15.451	0.000
	BRACE2035381	10.177	0.000
	BRACE2044286	18.667	0.000
	BRACE2045954	27.309	0.000
	BRACE3000787	32.844	0.000
15	BRACE3003192	58.488	0.000
	BRACE3005499	31.276	0.000
	BRACE3007480	19.471	0.000
	BRACE3009237	18.139	0.000
	BRACE3009724	58.488	0.000
20	BRACE3009747	2.237	8.327
	BRACE3010428	6.868	4.261
	BRACE3011271	11.036	0.000
	BRACE3011421	28.251	0.000
	BRACE3012364	8.506	0.000
25	BRACE3013780	0.000	17.852
	BRACE3022769	4.285	5.316
	BRACE3026735	24.173	0.000
	BRACE3031838	58.488	0.000
	BRALZ2011796	5.511	20.514
30	BRAMY2003008	26.445	0.000
	BRAMY2005052	11.612	0.000
	BRAMY2019300	49.811	0.000
	BRAMY2019963	20.428	0.000
	BRAMY2036567	7.474	0.000
35	BRAMY2037823	29.664	0.000
	BRAMY2040592	3.482	0.000

	BRAMY2047420	0.000	3.770
	BRAMY3002803	14.428	0.000
	BRAMY3004224	33.027	0.000
	BRAMY3005091	19.193	0.000
5	BRAWH1000127	15.983	35.693
	BRAWH2001395	14.290	12.514
	BRAWH2001671	7.605	0.000
	BRAWH2001940	37.398	0.000
	BRAWH2001973	37.398	0.000
10	BRAWH2002560	6.454	12.010
	BRAWH2002761	100.000	0.000
	BRAWH2005315	100.000	0.000
	BRAWH2007658	58.101	0.000
	BRAWH2010000	18.745	0.000
15	BRAWH2010084	100.000	0.000
	BRAWH2010536	14.718	0.000
	BRAWH2012162	36.060	0.000
	BRAWH2012326	100.000	0.000
	BRAWH2013294	39.442	0.000
20	BRAWH2013871	37.485	0.000
	BRAWH2014414	17.865	0.000
	BRAWH2014645	4.228	0.000
	BRAWH2014662	15.521	0.000
	BRAWH2014876	10.473	0.000
25	BRAWH2014954	58.488	0.000
	BRAWH2016221	47.417	0.000
	BRAWH2016439	100.000	0.000
	BRAWH2016702	73.807	0.000
	BRAWH2016724	35.119	0.000
30	BRAWH3000078	100.000	0.000
	BRAWH3000100	100.000	0.000
	BRAWH3000314	71.553	0.000
	BRAWH3000491	100.000	0.000
	BRAWH3001326	45.606	0.000
35	BRAWH3001475	100.000	0.000
	BRAWH3001891	34.539	0.000

	BRAWH3002574	13.222	0.000
	BRAWH3002600	36.800	0.000
	BRAWH3002819	100.000	0.000
	BRAWH3002821	21.953	0.000
5	BRAWH3003522	100.000	0.000
	BRAWH3003555	15.229	0.000
	BRAWH3003727	10.055	0.000
	BRAWH3003801	100.000	0.000
	BRAWH3003992	29.008	0.000
10	BRAWH3004453	100.000	0.000
	BRAWH3004666	49.499	0.000
	BRAWH3005132	49.811	0.000
	BRAWH3005422	100.000	0.000
	BRAWH3005912	100.000	0.000
15	BRAWH3005981	29.324	0.000
	BRAWH3006548	71.018	0.000
	BRAWH3006792	49.499	0.000
	BRAWH3007221	100.000	0.000
	BRAWH3007506	100.000	0.000
20	BRAWH3007592	8.966	0.000
	BRAWH3007726	54.530	0.000
	BRAWH3007783	100.000	0.000
	BRAWH3008341	100.000	0.000
	BRAWH3008697	100.000	0.000
25	BRAWH3008931	3.463	12.891
	BRAWH3009297	58.488	0.000
	BRCOC2003213	10.381	0.000
	BRCOC2014033	15.633	0.000
	BRCOC2020142	22.014	0.000
30	BRHIP2000920	36.630	0.000
	BRHIP2005719	49.499	0.000
	BRHIP2007741	6.943	0.000
	BRHIP2014228	29.439	0.000
	BRHIP2024146	3.042	10.190
35	BRHIP3000339	14.290	12.514
	BRHIP3006683	24.100	0.000

	BRHIP3007586	17.255	0.000
	BRHIP3008405	35.187	0.000
	BRHIP3018797	30.810	0.000
	BRSSN2000684	23.433	17.444
5	BRSSN2003086	0.000	100.000
	BRSSN2004496	0.000	78.696
	BRSSN2004719	0.000	39.002
	BRSSN2006892	0.000	57.631
	BRSSN2008549	0.000	63.611
10	BRSSN2008797	0.000	77.045
	BRSSN2011262	0.000	10.489
	BRSSN2011738	31.553	39.146
	BRSSN2013874	0.000	100.000
	BRSSN2014299	3.695	13.753
15	BRSSN2014424	0.000	61.866
	BRSSN2014556	0.000	100.000
	BRSSN2018581	0.000	50.137
	BRSSN2018925	0.000	100.000
	BRSTN2008052	32.844	0.000
20	BRSTN2015015	14.017	0.000
	BRSTN2016470	0.438	0.000
	BRTHA1000311	11.803	10.982
	BRTHA2003461	0.000	8.169
	BRTHA2008335	16.281	0.000
25	BRTHA3002427	8.577	10.641
	BRTHA3003490	1.623	0.000
	BRTHA3008520	47.417	0.000
	BRTHA3017848	47.417	0.000
	COLON2001721	11.065	0.000
30	CTONG2017500	2.649	0.000
	CTONG2028124	0.503	0.000
	CTONG3000657	3.880	0.000
	CTONG3001123	7.847	0.000
	CTONG3009328	11.993	0.000
35	FCBBF2001183	16.537	6.155
	FCBBF3001977	7.448	0.000

	FEBRA2007544	14.689	0.000
	FEBRA2007801	4.937	0.000
	FEBRA2020886	12.124	0.000
	FEBRA2024136	0.000	42.701
5	FEBRA2025427	0.000	9.226
	FEBRA2028618	5.082	0.000
	HCASM2007047	3.431	0.000
	HCHON2000244	0.658	0.000
	HCHON2000626	2.351	4.375
10	HCHON2001217	3.123	0.000
	HCHON2002676	13.647	0.000
	HCHON2006250	1.565	0.000
	HEART1000074	0.759	0.000
	HHDPC1000118	2.096	0.000
15	HLUNG2002465	1.209	0.000
	IMR322000127	3.098	0.000
	IMR322002035	36.176	0.000
	KIDNE2006580	7.013	0.000
	MESAN2006563	0.691	2.570
20	MESAN2012054	12.754	0.000
	MESTC1000042	2.245	0.000
	NOVAR2001783	4.027	0.000
	NT2NE2006909	0.285	0.000
	NT2RI2008724	1.836	0.000
25	NT2RI2012659	13.562	0.000
	NT2RI2014733	24.938	0.000
	NT2RI3002892	8.799	0.000
	NT2RI3006284	4.138	0.000
	NT2RI3006673	19.959	0.000
30	NT2RI3007543	1.697	0.000
	NT2RI3008055	44.179	0.000
	NT2RP7005529	14.766	0.000
	NT2RP7009147	14.337	0.000
	NT2RP7014005	5.818	0.000
35	NT2RP7017474	18.823	0.000
	OCBBF2001794	4.728	0.000

	OCBBF2006005	9.535	0.000
	OCBBF2006764	15.345	0.000
	OCBBF2007028	9.665	0.000
	OCBBF2010140	32.508	0.000
5	OCBBF2021286	18.456	0.000
	OCBBF2024850	4.445	0.000
	OCBBF2028935	5.789	8.618
	OCBBF2036743	11.053	0.000
	OCBBF2038317	19.713	0.000
10	OCBBF3000483	11.973	0.000
	OCBBF3008230	29.840	0.000
	PEBLM2004666	3.715	0.000
	PLACE6001185	21.358	0.000
	PUAEN2005930	18.362	0.000
15	PUAEN2006701	2.249	0.000
	PUAEN2007044	8.600	0.000
	PUAEN2009655	18.275	0.000
	SPLEN2028914	2.792	0.000
	SPLEN2031424	15.229	0.000
20	SPLEN2031547	1.574	0.000
	SPLEN2034781	27.984	0.000
	SPLEN2036932	2.932	0.000
	SYNOV2014400	12.977	0.000
	SYNOV4002346	5.997	0.000
25	SYNOV4002883	23.940	0.000
	SYNOV4007430	31.677	0.000
	SYNOV4008440	1.475	0.000
	TESOP2002451	2.375	0.000
	TESTI4000014	1.964	0.665
30	TESTI4000209	2.649	0.000
	TESTI4001100	4.098	0.000
	TESTI4006137	25.755	0.000
	TESTI4008797	12.429	0.000
	TESTI4009286	1.450	0.000
35	TESTI4010851	3.280	2.035
	TESTI4013817	27.163	0.000

	TESTI4014694	2.229	0.000
	TESTI4021478	22.098	0.000
	TESTI4022936	26.445	0.000
	TESTI4024420	37.398	0.000
5	TESTI4027821	60.471	0.000
	TESTI4037156	0.000	2.060
	THYMU2001090	21.252	0.000
	THYMU2033308	13.964	0.000
	THYMU2035735	1.319	0.000
10	THYMU2039315	54.530	0.000
	THYMU3001234	11.085	0.000
	THYMU3008171	20.170	0.000
	TKIDN2009641	5.782	21.519
	TKIDN2009889	35.077	0.000
15	TKIDN2015788	5.261	0.000
	TRACH1000205	19.677	0.000
	TRACH2001549	8.457	0.000
	TRACH2005811	2.109	0.000
	TRACH2006049	47.167	0.000
20	TRACH2007834	0.504	1.877
	TRACH2008300	10.186	0.000
	TRACH2025535	5.806	0.000
	TRACH3001427	5.571	0.000
	TRACH3002192	4.989	2.321
25	TRACH3004721	8.721	0.000
	TRACH3005294	7.428	0.000
	TRACH3007479	1.075	0.000
	TRACH3008093	2.449	0.000
	TRACH3009455	47.167	0.000
30	UTERU2006115	7.837	0.000
	UTERU2019706	45.606	0.000
	UTERU2023039	45.606	0.000
	UTERU2026203	45.606	0.000
	UTERU3005230	24.419	0.000
35	UTERU3007640	45.606	0.000
	UTERU3009871	36.230	0.000

	ADRGL2000042	2.540	18.905
	BLADE2006830	1.681	0.000
	BRACE2003609	9.090	0.000
	BRAMY3004800	38.061	0.000
5	BRAWH1000369	100.000	0.000
	BRAWH2006207	12.943	48.175
	BRAWH2006395	12.446	0.000
	BRAWH2008993	49.811	0.000
	BRAWH2009393	100.000	0.000
10	BRAWH2010552	58.488	0.000
	BRAWH3007441	100.000	0.000
	BRAWH3009017	100.000	0.000
	BRHIP2005271	7.083	0.000
	BRHIP3000017	8.819	0.000
15	BRTHA2018443	22.098	0.000
	BRTHA3003000	17.150	63.832
	CTONG2020374	31.081	0.000
	CTONG2020378	16.140	0.000
	CTONG2024031	2.584	0.000
20	FCBBF1000509	3.732	6.945
	FEBRA2001990	18.144	0.000
	FEBRA2006519	11.891	0.000
	FEBRA2028516	8.007	0.000
	HCHON2000743	6.105	0.000
25	IMR322001879	9.638	0.000
	NT2RI2009583	0.224	1.665
	OCBBF2008144	5.768	0.000
	PERIC2007068	3.086	0.000
	PUAEN2006335	12.682	0.000
30	SPLEN2039379	5.792	0.000
	TESTI2015626	0.000	1.224
	TESTI4001984	60.471	0.000
	TESTI400805^	8.814	0.000
	TESTI4025268	60.471	0.000
35	TESTI4032090	60.471	0.000
	THYMU3000360	39.314	0.000

TLIVE2002046	5.445	0.000
TRACH3000134	36.165	0.000
UTERU2021820	24.929	0.000
UTERU2028734	21.953	0.000

5

The result of comparative analysis of cDNA libraries derived from the hippocampus (BRHIP), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

10

Table 6

	Clone ID	BRAWH	BRHIP
15	ASTR01000009	2.611	0.000
	BLADE2001371	0.000	12.691
	BLADE2008398	12.401	18.978
	BNGH42007788	0.000	3.141
	BRACE1000186	4.324	2.206
20	BRACE1000258	31.956	0.000
	BRACE1000533	11.795	9.627
	BRACE2005457	58.488	0.000
	BRACE2010489	63.510	10.799
	BRACE2014657	15.451	0.000
25	BRACE2015058	0.000	8.947
	BRACE2018762	0.000	58.973
	BRACE2030341	0.000	7.057
	BRACE2035381	10.177	20.766
	BRACE2044286	18.667	0.000
30	BRACE2045954	27.309	0.000
	BRACE3000787	32.844	0.000
	BRACE3003192	58.488	0.000
	BRACE3005499	31.276	0.000
	BRACE3007480	19.471	52.973
35	BRACE3009237	18.139	37.013
	BRACE3009724	58.488	0.000

	BRACE3009747	2. 237	2. 283
	BRACE3010428	6. 868	2. 336
	BRACE3011271	11. 036	11. 259
	BRACE3011421	28. 251	0. 000
5	BRACE3012364	8. 506	4. 339
	BRACE3018963	0. 000	58. 973
	BRACE3022769	4. 285	4. 372
	BRACE3026735	24. 173	0. 000
	BRACE3031838	58. 488	0. 000
10	BRALZ2011796	5. 511	0. 000
	BRAMY2003008	26. 445	0. 000
	BRAMY2005052	11. 612	0. 000
	BRAMY2019300	49. 811	0. 000
	BRAMY2019963	20. 428	6. 947
15	BRAMY2031317	0. 000	16. 004
	BRAMY2036567	7. 474	7. 626
	BRAMY2037823	29. 664	0. 000
	BRAMY2040592	3. 482	7. 105
	BRAMY2044078	0. 000	8. 947
20	BRAMY3002803	14. 428	44. 161
	BRAMY3004224	33. 027	33. 695
	BRAMY3005091	19. 193	0. 000
	BRAMY3009811	0. 000	66. 943
	BRAWH1000127	15. 983	3. 261
25	BRAWH2001395	14. 290	22. 297
	BRAWH2001671	7. 605	11. 638
	BRAWH2001940	37. 398	38. 155
	BRAWH2001973	37. 398	38. 155
	BRAWH2002560	6. 454	3. 292
30	BRAWH2002761	100. 000	0. 000
	BRAWH2005315	100. 000	0. 000
	BRAWH2007658	58. 101	0. 000
	BRAWH2010000	1°. 745	3°. 249
	BRAWH2010084	100. 000	0. 000
35	BRAWH2010536	14. 718	0. 000
	BRAWH2012162	36. 060	0. 000

	BRAWH2012326	100.000	0.000
	BRAWH2013294	39.442	10.060
	BRAWH2013871	37.485	0.000
	BRAWH2014414	17.865	18.227
5	BRAWH2014645	4.228	1.078
	BRAWH2014662	15.521	0.000
	BRAWH2014876	10.473	0.000
	BRAWH2014954	58.488	0.000
	BRAWH2016221	47.417	0.000
10	BRAWH2016439	100.000	0.000
	BRAWH2016702	73.807	0.000
	BRAWH2016724	35.119	0.000
	BRAWH3000078	100.000	0.000
	BRAWH3000100	100.000	0.000
15	BRAWH3000314	71.553	0.000
	BRAWH3000491	100.000	0.000
	BRAWH3001326	45.606	0.000
	BRAWH3001475	100.000	0.000
	BRAWH3001891	34.539	0.000
20	BRAWH3002574	13.222	0.000
	BRAWH3002600	36.800	0.000
	BRAWH3002819	100.000	0.000
	BRAWH3002821	21.953	0.000
	BRAWH3003522	100.000	0.000
25	BRAWH3003555	15.229	0.000
	BRAWH3003727	10.055	10.259
	BRAWH3003801	100.000	0.000
	BRAWH3003992	29.008	0.000
	BRAWH3004453	100.000	0.000
30	BRAWH3004666	49.499	50.501
	BRAWH3005132	49.811	0.000
	BRAWH3005422	100.000	0.000
	BRAWH3005912	100.000	0.000
	BRAWH3005981	29.324	0.000
35	BRAWH3006548	71.018	28.982
	BRAWH3006792	49.499	50.501

	BRAWH3007221	100.000	0.000
	BRAWH3007506	100.000	0.000
	BRAWH3007592	8.966	3.659
	BRAWH3007726	54.530	0.000
5	BRAWH3007783	100.000	0.000
	BRAWH3008341	100.000	0.000
	BRAWH3008697	100.000	0.000
	BRAWH3008931	3.463	10.601
	BRAWH3009297	58.488	0.000
10	BRCAN2020710	0.000	22.176
	BRCAN2028355	0.000	1.507
	BRCOC2003213	10.381	0.000
	BRCOC2014033	15.633	15.950
	BRCOC2020142	22.014	0.000
15	BRHIP2000691	0.000	100.000
	BRHIP2000819	0.000	2.204
	BRHIP2000826	0.000	100.000
	BRHIP2000920	36.630	37.371
	BRHIP2001074	0.000	39.976
20	BRHIP2001805	0.000	14.757
	BRHIP2001927	0.000	100.000
	BRHIP2002122	0.000	100.000
	BRHIP2002172	0.000	100.000
	BRHIP2002346	0.000	100.000
25	BRHIP2003242	0.000	100.000
	BRHIP2003786	0.000	100.000
	BRHIP2003917	0.000	11.981
	BRHIP2004312	0.000	100.000
	BRHIP2004359	0.000	24.839
30	BRHIP2004814	0.000	35.391
	BRHIP2004883	0.000	100.000
	BRHIP2005236	0.000	100.000
	BRHIP2005354	0.000	100.000
	BRHIP2005600	0.000	100.000
35	BRHIP2005719	49.499	50.501
	BRHIP2005752	0.000	58.973

	BRHIP2005932	0.000	100.000
	BRHIP2006800	0.000	100.000
	BRHIP2007616	0.000	100.000
	BRHIP2007741	6.943	3.542
5	BRHIP2009340	0.000	100.000
	BRHIP2009414	0.000	100.000
	BRHIP2009474	0.000	47.917
	BRHIP2013699	0.000	21.770
	BRHIP2014228	29.439	15.017
10	BRHIP2021615	0.000	100.000
	BRHIP2022221	0.000	47.917
	BRHIP2024146	3.042	5.897
	BRHIP2024165	0.000	100.000
	BRHIP2026061	0.000	31.199
15	BRHIP2026288	0.000	22.018
	BRHIP2029176	0.000	100.000
	BRHIP2029393	0.000	100.000
	BRHIP3000339	14.290	22.297
	BRHIP3000526	0.000	100.000
20	BRHIP3001283	0.000	50.312
	BRHIP3006683	24.100	49.175
	BRHIP3007483	0.000	100.000
	BRHIP3007586	17.255	24.645
	BRHIP3008183	0.000	100.000
25	BRHIP3008313	0.000	29.118
	BRHIP3008344	0.000	46.104
	BRHIP3008405	35.187	17.949
	BRHIP3008565	0.000	46.104
	BRHIP3008598	0.000	100.000
30	BRHIP3008997	0.000	100.000
	BRHIP3009099	0.000	35.577
	BRHIP3009448	0.000	100.000
	BRHIP3011241	0.000	100.000
	BRHIP3013765	0.000	100.000
35	BRHIP3013897	0.000	100.000
	BRHIP3015751	0.000	100.000

	BRHIP3016213	0.000	100.000
	BRHIP3018797	30.810	9.567
	BRHIP3020182	0.000	100.000
	BRHIP3024118	0.000	100.000
5	BRHIP3024533	0.000	100.000
	BRHIP3024725	0.000	100.000
	BRHIP3025161	0.000	100.000
	BRHIP3025702	0.000	100.000
	BRHIP3026097	0.000	100.000
10	BRHIP3027137	0.000	100.000
	BRHIP3027854	0.000	100.000
	BRSSN2000684	23.433	19.126
	BRSSN2004719	0.000	10.691
	BRSSN2008549	0.000	17.436
15	BRSSN2011738	31.553	0.000
	BRSSN2014299	3.695	3.770
	BRSTN2008052	32.844	0.000
	BRSTN2015015	14.017	0.000
	BRSTN2016470	0.438	0.447
20	BRSTN2018083	0.000	22.055
	BRTHA1000311	11.803	6.021
	BRTHA2002442	0.000	31.507
	BRTHA2008335	16.281	8.305
	BRTHA3000297	0.000	47.917
25	BRTHA3001721	0.000	12.017
	BRTHA3002427	8.577	2.917
	BRTHA3003490	1.623	0.000
	BRTHA3005046	0.000	47.917
	BRTHA3008520	47.417	0.000
30	BRTHA3008778	0.000	25.346
	BRTHA3009090	0.000	12.008
	BRTHA3015910	0.000	15.221
	BRTHA3017848	47.417	0.000
	COLON2001721	11.065	5.644
35	CTONG1000087	0.000	1.067
	CTONG1000088	0.000	2.981

	CTONG1000467	0.000	8.766
	CTONG2000042	0.000	3.574
	CTONG2008233	0.000	0.701
	CTONG2009423	0.000	35.391
5	CTONG2017500	2.649	0.000
	CTONG2019788	0.000	3.120
	CTONG2028124	0.503	1.026
	CTONG3000657	3.880	11.875
	CTONG3001123	7.847	0.000
10	CTONG3001370	0.000	3.574
	CTONG3002412	0.000	10.918
	CTONG3004072	0.000	19.915
	CTONG3008894	0.000	2.966
	CTONG3009239	0.000	2.946
15	CTONG3009328	11.993	0.000
	DFNES2011499	0.000	6.330
	FCBBF2001183	16.537	11.810
	FCBBF3001977	7.448	7.599
	FEBRA2000253	0.000	14.934
20	FEBRA2007544	14.689	4.995
	FEBRA2007801	4.937	7.556
	FEBRA2008287	0.000	3.007
	FEBRA2010719	0.000	17.703
	FEBRA2020886	12.124	12.369
25	FEBRA2028618	5.082	0.000
	HCASM2007047	3.431	0.000
	HCHON2000028	0.000	1.619
	HCHON2000244	0.658	0.671
	HCHON2000626	2.351	0.000
30	HCHON2001217	3.123	2.124
	HCHON2002676	13.647	0.000
	HCHON2005921	0.000	12.694
	HCHON2006250	1.565	0.000
	HEART1000074	0.759	0.000
35	HEART2007031	0.000	11.593
	HHDPC1000118	2.096	6.415

	HLUNG2002465	1.209	3.702
	HLUNG2003003	0.000	16.306
	IMR322000127	3.098	3.161
	IMR322001380	0.000	2.022
5	IMR322002035	36.176	0.000
	KIDNE2005543	0.000	18.168
	KIDNE2006580	7.013	14.310
	MESAN2006563	0.691	0.000
	MESAN2012054	12.754	15.615
10	MESTC1000042	2.245	0.000
	NOVAR2001783	4.027	0.000
	NT2NE2006909	0.285	0.000
	NT2RI2008724	1.836	1.874
	NT2RI2012659	13.562	0.000
15	NT2RI2014733	24.938	0.000
	NT2RI2018311	0.000	21.918
	NT2RI3001515	0.000	11.050
	NT2RI3002892	8.799	16.159
	NT2RI3004510	0.000	28.761
20	NT2RI3005724	0.000	12.093
	NT2RI3006284	4.138	0.000
	NT2RI3006673	19.959	10.182
	NT2RI3007291	0.000	12.770
	NT2RI3007543	1.697	0.866
25	NT2RI3008055	44.179	0.000
	NT2RP7005529	14.766	15.065
	NT2RP7009147	14.337	1.625
	NT2RP7014005	5.818	0.000
	NT2RP7017474	18.823	0.000
30	OCBBF2001794	4.728	0.000
	OCBBF2003819	0.000	21.496
	OCBBF2006005	9.535	9.728
	OCBBF2006151	0.000	11.764
	OCBBF2006764	15.345	0.000
35	OCBBF2007028	9.665	11.269
	OCBBF2007068	0.000	45.093

	OCBBF2010140	32.508	0.000
	OCBBF2020741	0.000	28.789
	OCBBF2021286	18.456	18.829
	OCBBF2024719	0.000	30.261
5	OCBBF2024850	4.445	4.535
	OCBBF2028935	5.789	7.087
	OCBBF2036743	11.053	0.000
	OCBBF2038317	19.713	0.000
	OCBBF3000296	0.000	19.328
10	OCBBF3000483	11.973	8.143
	OCBBF3008230	29.840	0.000
	PEBLM2004666	3.715	0.000
	PLACE6001185	21.358	0.000
	PUAEN2005930	18.362	9.367
15	PUAEN2006701	2.249	2.295
	PUAEN2007044	8.600	0.000
	PUAEN2009655	18.275	7.458
	SPLEN2010912	0.000	12.636
	SPLEN2012624	0.000	10.317
20	SPLEN2028914	2.792	0.000
	SPLEN2031424	15.229	0.000
	SPLEN2031547	1.574	11.244
	SPLEN2034781	27.984	0.000
	SPLEN2036932	2.932	5.982
25	SYNOV2014400	12.977	13.240
	SYNOV4002346	5.997	0.000
	SYNOV4002883	23.940	24.425
	SYNOV4007430	31.677	0.000
	SYNOV4008440	1.475	3.010
30	TESOP2002451	2.375	0.000
	TESTI2049246	0.000	53.653
	TESTI4000014	1.964	2.551
	TESTI4000209	2.649	0.000
	TESTI4001100	4.098	4.180
35	TESTI4006137	25.755	0.000
	TESTI4008797	12.429	12.681

	TESTI4009286	1.450	1.479
	TESTI4010377	0.000	60.949
	TESTI4010851	3.280	3.904
	TESTI4010928	0.000	34.221
5	TESTI4011161	0.000	21.496
	TESTI4013817	27.163	27.712
	TESTI4014159	0.000	23.916
	TESTI4014694	2.229	0.000
	TESTI4014818	0.000	60.949
10	TESTI4021478	22.098	0.000
	TESTI4022936	26.445	0.000
	TESTI4024420	37.398	38.155
	TESTI4027821	60.471	0.000
	TESTI4037156	0.000	0.282
15	THYMU2001090	21.252	0.000
	THYMU2023967	0.000	31.165
	THYMU2025707	0.000	9.440
	THYMU2031341	0.000	7.040
	THYMU2033308	13.964	0.000
20	THYMU2035735	1.319	2.692
	THYMU2037226	0.000	34.964
	THYMU2039315	54.530	0.000
	THYMU3001234	11.085	0.000
	THYMU3001379	0.000	25.695
25	THYMU3004835	0.000	20.041
	THYMU3007137	0.000	37.956
	THYMU3008171	20.170	20.579
	TKIDN2009641	5.782	0.000
	TKIDN2009889	35.077	0.000
30	TKIDN2015788	5.261	2.684
	TRACH1000205	19.677	4.015
	TRACH2001549	8.457	21.569
	TRACH2005811	2.109	2.152
	TRACH2006049	47.167	0.000
35	TRACH2007834	0.504	0.515
	TRACH2008300	10.186	13.857

	TRACH2025535	5.806	2.369
	TRACH3000014	0.000	18.547
	TRACH3001427	5.571	2.842
	TRACH3002192	4.989	6.999
5	TRACH3004721	8.721	2.966
	TRACH3005294	7.428	0.000
	TRACH3007479	1.075	0.000
	TRACH3008093	2.449	0.000
	TRACH3009455	47.167	0.000
10	TUTER1000122	0.000	3.330
	TUTER2000904	0.000	5.697
	UTERU2004929	0.000	11.843
	UTERU2006115	7.837	0.000
	UTERU2019706	45.606	0.000
15	UTERU2021163	0.000	46.104
	UTERU2023039	45.606	0.000
	UTERU2026203	45.606	0.000
	UTERU2030213	0.000	25.133
	UTERU3001572	0.000	1.862
20	UTERU3003135	0.000	33.486
	UTERU3005230	24.419	0.000
	UTERU3007640	45.606	0.000
	UTERU3009259	0.000	46.104
	UTERU3009871	36.230	18.482
25	ADRGL2000042	2.540	0.000
	BLADE2006830	1.681	0.000
	BRACE2003609	9.090	0.000
	BRAMY3004800	38.061	46.598
	BRAWH1000369	100.000	0.000
30	BRAWH2006207	12.943	0.000
	BRAWH2006395	12.446	0.000
	BRAWH2008993	49.811	0.000
	BRAWH2009393	100.000	0.000
	BRAWH2010552	58.488	0.000
35	BRAWH3007441	100.000	0.000
	BRAWH3009017	100.000	0.000

	BRHIP2002722	0.000	100.000
	BRHIP2003272	0.000	100.000
	BRHIP2005271	7.083	14.453
	BRHIP2005724	0.000	100.000
5	BRHIP2006617	0.000	100.000
	BRHIP2008389	0.000	100.000
	BRHIP2012360	0.000	100.000
	BRHIP2017553	0.000	100.000
	BRHIP2026877	0.000	30.781
10	BRHIP3000017	8.819	4.499
	BRHIP3000240	0.000	32.393
	BRHIP3008314	0.000	100.000
	BRHIP3026052	0.000	45.860
	BRTA2018443	22.098	0.000
15	BRTA3003000	17.150	0.000
	CTONG2020374	31.081	0.000
	CTONG2020378	16.140	16.467
	CTONG2024031	2.584	0.000
	CTONG3004726	0.000	17.278
20	FCBBF1000509	3.732	5.711
	FEBRA2001990	18.144	7.404
	FEBRA2006519	11.891	0.000
	FEBRA2028516	8.007	4.668
	HCHON2000743	6.105	0.000
25	IMR322001879	9.638	9.833
	NT2RI2009583	0.224	0.228
	OCBBF2006987	0.000	13.187
	OCBBF2008144	5.768	2.942
	OCBBF2030116	0.000	45.093
30	PERIC2007068	3.086	4.723
	PUAEN2006335	12.682	0.000
	SPLEN2039379	5.792	8.864
	TESTI2015626	0.000	0.336
	TESTI4000214	0.000	7.979
35	TESTI4001984	60.471	0.000
	TESTI4008058	8.814	0.000

	TESTI4013894	0.000	14.289
	TESTI4025268	60.471	0.000
	TESTI4025547	0.000	60.949
	TESTI4026207	0.000	60.949
5	TESTI4032090	60.471	0.000
	THYMU3000360	39.314	0.000
	TLIVE2002046	5.445	1.852
	TRACH3000134	36.165	0.000
	UTERU2008040	0.000	24.014
10	UTERU2021820	24.929	0.000
	UTERU2028734	21.953	0.000

The result of comparative analysis of cDNA libraries derived from the cerebellum (BRACE), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 7

	Clone ID	BRAWH	BRACE
	ADRGL2009146	0.000	10.913
	ADRGL2012038	0.000	1.459
	ASTR01000009	2.611	0.000
25	ASTR02003960	0.000	17.003
	BLADE1000176	0.000	16.822
	BLADE2004089	0.000	7.034
	BLADE2008398	12.401	4.401
	BRACE1000186	4.324	1.535
30	BRACE1000258	31.956	68.044
	BRACE1000533	11.795	11.720
	BRACE1000572	0.000	100.000
	BRACE2003639	0.000	100.000
	BRACE2005457	58.488	41.512
35	BRACE2006319	0.000	4.977
	BRACE2008594	0.000	100.000

	BRACE2010489	63.510	15.026
	BRACE2011747	0.000	100.000
	BRACE2014306	0.000	6.909
	BRACE2014475	0.000	100.000
5	BRACE2014657	15.451	76.765
	BRACE2015058	0.000	6.224
	BRACE2015314	0.000	100.000
	BRACE2016981	0.000	16.089
	BRACE2018762	0.000	41.027
10	BRACE2024627	0.000	8.689
	BRACE2026836	0.000	4.898
	BRACE2027258	0.000	23.981
	BRACE2027970	0.000	45.981
	BRACE2028970	0.000	100.000
15	BRACE2029112	0.000	100.000
	BRACE2029849	0.000	100.000
	BRACE2030326	0.000	100.000
	BRACE2030341	0.000	4.909
	BRACE2030884	0.000	100.000
20	BRACE2031154	0.000	39.025
	BRACE2031389	0.000	7.220
	BRACE2031527	0.000	100.000
	BRACE2031531	0.000	100.000
	BRACE2031899	0.000	100.000
25	BRACE2032044	0.000	100.000
	BRACE2032329	0.000	100.000
	BRACE2032385	0.000	100.000
	BRACE2032538	0.000	100.000
	BRACE2032823	0.000	100.000
30	BRACE2033720	0.000	100.000
	BRACE2035381	10.177	36.117
	BRACE2035441	0.000	100.000
	BRACE2036005	0.000	100.000
	BRACE2036096	0.000	100.000
35	BRACE2036830	0.000	100.000
	BRACE2036834	0.000	100.000

	BRACE2037847	0.000	100.000
	BRACE2038114	0.000	100.000
	BRACE2038329	0.000	100.000
	BRACE2038551	0.000	100.000
5	BRACE2039249	0.000	100.000
	BRACE2039327	0.000	100.000
	BRACE2039475	0.000	100.000
	BRACE2039734	0.000	100.000
	BRACE2040138	0.000	100.000
10	BRACE2040325	0.000	100.000
	BRACE2041009	0.000	100.000
	BRACE2041200	0.000	38.787
	BRACE2041264	0.000	100.000
	BRACE2042550	0.000	100.000
15	BRACE2043142	0.000	52.057
	BRACE2043248	0.000	100.000
	BRACE2043349	0.000	100.000
	BRACE2043665	0.000	16.915
	BRACE2044286	18.667	26.499
20	BRACE2044816	0.000	100.000
	BRACE2044949	0.000	2.766
	BRACE2045300	0.000	100.000
	BRACE2045428	0.000	100.000
	BRACE2045596	0.000	100.000
25	BRACE2045772	0.000	2.055
	BRACE2045947	0.000	100.000
	BRACE2045954	27.309	38.766
	BRACE2046251	0.000	100.000
	BRACE2046295	0.000	100.000
30	BRACE2047011	0.000	100.000
	BRACE2047350	0.000	45.981
	BRACE2047377	0.000	100.000
	BRACE20473°5	0.000	100.000
	BRACE3000071	0.000	9.532
35	BRACE3000697	0.000	100.000
	BRACE3000787	32.844	15.541

	BRACE3000840	0.000	100.000
	BRACE3000973	0.000	28.699
	BRACE3001002	0.000	100.000
	BRACE3001217	0.000	100.000
5	BRACE3001391	0.000	100.000
	BRACE3001595	0.000	100.000
	BRACE3001754	0.000	38.787
	BRACE3002298	0.000	100.000
	BRACE3002390	0.000	100.000
10	BRACE3002508	0.000	100.000
	BRACE3003004	0.000	100.000
	BRACE3003192	58.488	41.512
	BRACE3003595	0.000	100.000
	BRACE3003698	0.000	45.981
15	BRACE3004058	0.000	100.000
	BRACE3004113	0.000	100.000
	BRACE3004150	0.000	2.757
	BRACE3004358	0.000	100.000
	BRACE3004435	0.000	100.000
20	BRACE3004772	0.000	100.000
	BRACE3004783	0.000	100.000
	BRACE3004843	0.000	22.581
	BRACE3004880	0.000	100.000
	BRACE3005145	0.000	100.000
25	BRACE3005225	0.000	100.000
	BRACE3005430	0.000	100.000
	BRACE3005499	31.276	22.199
	BRACE3006185	0.000	100.000
	BRACE3006226	0.000	100.000
30	BRACE3006462	0.000	100.000
	BRACE3006872	0.000	100.000
	BRACE3007322	0.000	100.000
	BRACE3007472	0.000	100.000
	BRACE3007480	19.471	13.820
35	BRACE3007559	0.000	100.000
	BRACE3007625	0.000	100.000

	BRACE3007642	0.000	100.000
	BRACE3007767	0.000	100.000
	BRACE3008036	0.000	13.098
	BRACE3008092	0.000	100.000
5	BRACE3008137	0.000	100.000
	BRACE3008384	0.000	56.141
	BRACE3008720	0.000	100.000
	BRACE3008772	0.000	37.308
	BRACE3009090	0.000	100.000
10	BRACE3009237	18.139	12.875
	BRACE3009297	0.000	100.000
	BRACE3009377	0.000	100.000
	BRACE3009574	0.000	100.000
	BRACE3009701	0.000	100.000
15	BRACE3009708	0.000	100.000
	BRACE3009724	58.488	41.512
	BRACE3009747	2.237	1.588
	BRACE3010397	0.000	24.243
	BRACE3010428	6.868	3.250
20	BRACE3011271	11.036	39.165
	BRACE3011421	28.251	40.103
	BRACE3011505	0.000	100.000
	BRACE3012364	8.506	6.038
	BRACE3012930	0.000	38.787
25	BRACE3013119	0.000	100.000
	BRACE3013576	0.000	100.000
	BRACE3013740	0.000	100.000
	BRACE3013780	0.000	3.404
	BRACE3014005	0.000	100.000
30	BRACE3014068	0.000	100.000
	BRACE3014231	0.000	100.000
	BRACE3014317	0.000	100.000
	BRACE3014807	0.000	100.000
	BRACE3015027	0.000	9.209
35	BRACE3015121	0.000	100.000
	BRACE3015262	0.000	100.000

	BRACE3015521	0.000	100.000
	BRACE3015894	0.000	100.000
	BRACE3016884	0.000	9.165
	BRACE3018308	0.000	100.000
5	BRACE3018963	0.000	41.027
	BRACE3019055	0.000	100.000
	BRACE3019084	0.000	100.000
	BRACE3020194	0.000	100.000
	BRACE3020286	0.000	100.000
10	BRACE3020594	0.000	100.000
	BRACE3022769	4.285	9.124
	BRACE3023912	0.000	100.000
	BRACE3024073	0.000	100.000
	BRACE3024659	0.000	100.000
15	BRACE3024662	0.000	100.000
	BRACE3025153	0.000	100.000
	BRACE3025457	0.000	100.000
	BRACE3025531	0.000	100.000
	BRACE3025630	0.000	100.000
20	BRACE3026008	0.000	100.000
	BRACE3026075	0.000	100.000
	BRACE3026735	24.173	51.471
	BRACE3027242	0.000	100.000
	BRACE3027326	0.000	100.000
25	BRACE3027478	0.000	11.360
	BRACE3030103	0.000	100.000
	BRACE3031838	58.488	41.512
	BRACE3032983	0.000	100.000
	BRACE3040856	0.000	100.000
30	BRACE3045033	0.000	100.000
	BRALZ2011796	5.511	3.912
	BRAMY2003008	26.445	0.000
	BRAMY2005052	11.612	8.242
	BRAMY2019300	49.811	0.000
35	BRAMY2019963	20.428	0.000
	BRAMY2020058	0.000	19.826

	BRAMY2030098	0.000	29.935
	BRAMY2031317	0.000	33.400
	BRAMY2036567	7.474	26.525
	BRAMY2037823	29.664	21.055
5	BRAMY2039872	0.000	14.071
	BRAMY2040592	3.482	0.000
	BRAMY2044078	0.000	6.224
	BRAMY2047420	0.000	0.719
	BRAMY3002620	0.000	41.329
10	BRAMY3002803	14.428	0.000
	BRAMY3004224	33.027	0.000
	BRAMY3005091	19.193	13.622
	BRAMY3005932	0.000	41.329
	BRAMY4000229	0.000	25.113
15	BRAWH1000127	15.983	4.538
	BRAWH2001395	14.290	3.580
	BRAWH2001671	7.605	8.097
	BRAWH2001940	37.398	0.000
	BRAWH2001973	37.398	0.000
20	BRAWH2002560	6.454	0.000
	BRAWH2002761	100.000	0.000
	BRAWH2005315	100.000	0.000
	BRAWH2007658	58.101	0.000
	BRAWH2010000	18.745	0.000
25	BRAWH2010084	100.000	0.000
	BRAWH2010536	14.718	0.000
	BRAWH2012162	36.060	0.000
	BRAWH2012326	100.000	0.000
	BRAWH2013294	39.442	13.997
30	BRAWH2013871	37.485	0.000
	BRAWH2014414	17.865	0.000
	BRAWH2014645	4.228	3.751
	BRAWH2014662	15.521	11.016
	BRAWH2014876	10.473	7.433
35	BRAWH2014954	58.488	41.512
	BRAWH2016221	47.417	0.000

	BRAWH2016439	100.000	0.000
	BRAWH2016702	73.807	26.193
	BRAWH2016724	35.119	0.000
	BRAWH3000078	100.000	0.000
5	BRAWH3000100	100.000	0.000
	BRAWH3000314	71.553	0.000
	BRAWH3000491	100.000	0.000
	BRAWH3001326	45.606	0.000
	BRAWH3001475	100.000	0.000
10	BRAWH3001891	34.539	36.772
	BRAWH3002574	13.222	0.000
	BRAWH3002600	36.800	26.120
	BRAWH3002819	100.000	0.000
	BRAWH3002821	21.953	0.000
15	BRAWH3003522	100.000	0.000
	BRAWH3003555	15.229	5.405
	BRAWH3003727	10.055	21.411
	BRAWH3003801	100.000	0.000
	BRAWH3003992	29.008	0.000
20	BRAWH3004453	100.000	0.000
	BRAWH3004666	49.499	0.000
	BRAWH3005132	49.811	0.000
	BRAWH3005422	100.000	0.000
	BRAWH3005912	100.000	0.000
25	BRAWH3005981	29.324	0.000
	BRAWH3006548	71.018	0.000
	BRAWH3006792	49.499	0.000
	BRAWH3007221	100.000	0.000
	BRAWH3007506	100.000	0.000
30	BRAWH3007592	8.966	6.364
	BRAWH3007726	54.530	0.000
	BRAWH3007783	100.000	0.000
	BRAWH3008341	100.000	0.000
	BRAWH3008697	100.000	0.000
35	BRAWH3008931	3.463	4.916
	BRAWH3009297	58.488	41.512

	BRCAN2009432	0.000	1.869
	BRCAN2010376	0.000	23.627
	BRCAN2015371	0.000	15.560
	BRCAN2020710	0.000	7.714
5	BRCOC2003213	10.381	7.368
	BRCOC2007034	0.000	16.691
	BRCOC2014033	15.633	0.000
	BRCOC2020142	22.014	0.000
	BRHIP2000920	36.630	25.999
10	BRHIP2004359	0.000	34.560
	BRHIP2005719	49.499	0.000
	BRHIP2005752	0.000	41.027
	BRHIP2007741	6.943	3.696
	BRHIP2013699	0.000	15.145
15	BRHIP2014228	29.439	10.447
	BRHIP2024146	3.042	0.864
	BRHIP3000339	14.290	3.580
	BRHIP3006683	24.100	0.000
	BRHIP3007586	17.255	7.348
20	BRHIP3008313	0.000	20.257
	BRHIP3008405	35.187	12.487
	BRHIP3018797	30.810	3.803
	BRSSN2000684	23.433	0.000
	BRSSN2006892	0.000	10.990
25	BRSSN2011262	0.000	2.000
	BRSSN2011738	31.553	7.465
	BRSSN2014299	3.695	2.623
	BRSTN2008052	32.844	15.541
	BRSTN2010750	0.000	7.220
30	BRSTN2015015	14.017	19.897
	BRSTN2016470	0.438	7.146
	BRTHA1000311	11.803	10.472
	BRTHA2008335	16.281	0.000
	BRTHA2008955	0.000	39.025
35	BRTHA2011194	0.000	39.025
	BRTHA3001721	0.000	8.360

	BRTHA3002427	8.577	2.029
	BRTHA3003490	1.623	2.304
	BRTHA3008520	47.417	0.000
	BRTHA3009090	0.000	8.354
5	BRTHA3017848	47.417	0.000
	COLON2001721	11.065	19.633
	CTONG2008233	0.000	3.412
	CTONG2017500	2.649	0.000
	CTONG2028124	0.503	2.854
10	CTONG3000657	3.880	5.508
	CTONG3001123	7.847	0.000
	CTONG3005813	0.000	27.592
	CTONG3008894	0.000	1.032
	CTONG3009328	11.993	0.000
15	DFNES2011499	0.000	4.403
	FCBBF2001183	16.537	5.869
	FCBBF3001977	7.448	10.573
	FEBRA2006396	0.000	5.705
	FEBRA2007544	14.689	41.703
20	FEBRA2007708	0.000	6.066
	FEBRA2007801	4.937	1.752
	FEBRA2008287	0.000	4.184
	FEBRA2020886	12.124	0.000
	FEBRA2021966	0.000	3.062
25	FEBRA2026984	0.000	12.446
	FEBRA2028618	5.082	10.821
	HCASM2007047	3.431	0.000
	HCHON2000244	0.658	0.934
	HCHON2000626	2.351	0.834
30	HCHON2001217	3.123	2.216
	HCHON2002676	13.647	0.000
	HCHON2005921	0.000	2.944
	HCHON2006250	1.565	0.000
	HEART1000074	0.759	1.078
35	HHDPC1000118	2.096	0.000
	HLUNG2002465	1.209	0.000

	IMR322000127	3.098	4.398
	IMR322001380	0.000	2.814
	IMR322002035	36.176	0.000
	KIDNE2000665	0.000	1.374
5	KIDNE2006580	7.013	14.933
	MESAN2006563	0.691	1.470
	MESAN2012054	12.754	5.432
	MESTC1000042	2.245	0.797
	NB9N41000340	0.000	2.059
10	NESOP2001752	0.000	3.228
	NOVAR2001783	4.027	0.000
	NT2NE2006909	0.285	0.000
	NT2RI2005166	0.000	18.511
	NT2RI2008724	1.836	0.000
15	NT2RI2012659	13.562	48.128
	NT2RI2014733	24.938	0.000
	NT2RI2019751	0.000	28.087
	NT2RI3002892	8.799	9.992
	NT2RI3003382	0.000	28.087
20	NT2RI3004510	0.000	20.009
	NT2RI3005724	0.000	42.065
	NT2RI3006284	4.138	1.469
	NT2RI3006673	19.959	0.000
	NT2RI3007291	0.000	35.535
25	NT2RI3007543	1.697	1.204
	NT2RI3008055	44.179	15.678
	NT2RP7004123	0.000	1.362
	NT2RP7005529	14.766	5.240
	NT2RP7009147	14.337	0.000
30	NT2RP7010599	0.000	22.750
	NT2RP7014005	5.818	0.000
	NT2RP7017474	18.823	13.360
	NTONG2005969	0.000	4.560
	OCBBF2001794	4.728	0.000
35	OCBBF2003819	0.000	14.955
	OCBBF2006005	9.535	0.000

	OCBBF2006151	0.000	4.092
	OCBBF2006764	15.345	21.782
	OCBBF2007028	9.665	8.820
	OCBBF2010140	32.508	0.000
5	OCBBF2020343	0.000	36.360
	OCBBF2020741	0.000	20.028
	OCBBF2021286	18.456	6.550
	OCBBF2022351	0.000	36.360
	OCBBF2024850	4.445	1.577
10	OCBBF2025527	0.000	36.360
	OCBBF2028935	5.789	1.643
	OCBBF2036743	11.053	15.690
	OCBBF2038317	19.713	0.000
	OCBBF3000483	11.973	14.163
15	OCBBF3007516	0.000	2.684
	OCBBF3008230	29.840	0.000
	PEBLM2004666	3.715	0.000
	PERIC2000889	0.000	6.314
	PLACE6001185	21.358	15.159
20	PUAEN2002489	0.000	9.262
	PUAEN2005930	18.362	0.000
	PUAEN2006701	2.249	0.000
	PUAEN2007044	8.600	5.087
	PUAEN2009655	18.275	0.000
25	SPLEN2010912	0.000	26.371
	SPLEN2012624	0.000	7.178
	SPLEN2027268	0.000	14.361
	SPLEN2028914	2.792	0.000
	SPLEN2031424	15.229	5.405
30	SPLEN2031547	1.574	5.587
	SPLEN2034781	27.984	0.000
	SPLEN2036932	2.932	2.081
	SPLEN2037194	0.000	28.977
	SYNOV2014400	12.977	0.000
35	SYNOV4002346	5.997	0.000
	SYNOV4002883	23.940	0.000

	SYNOV4007430	31.677	0.000
	SYNOV4007671	0.000	0.520
	SYNOV4008440	1.475	2.094
	TESOP2002273	0.000	2.881
5	TESOP2002451	2.375	3.372
	TESOP2002950	0.000	9.399
	TESTI1000330	0.000	52.057
	TESTI4000014	1.964	2.028
	TESTI4000209	2.649	0.000
10	TESTI4000349	0.000	36.899
	TESTI4001100	4.098	8.725
	TESTI4001561	0.000	28.578
	TESTI4006137	25.755	0.000
	TESTI4008797	12.429	0.000
15	TESTI4009286	1.450	0.000
	TESTI4010851	3.280	2.716
	TESTI4011161	0.000	14.955
	TESTI4013675	0.000	14.015
	TESTI4013817	27.163	0.000
20	TESTI4014159	0.000	16.638
	TESTI4014306	0.000	52.057
	TESTI4014694	2.229	0.791
	TESTI4021478	22.098	0.000
	TESTI4022936	26.445	0.000
25	TESTI4024420	37.398	0.000
	TESTI4027821	60.471	0.000
	TESTI4037156	0.000	0.982
	TESTI4046819	0.000	14.013
	THYMU2001090	21.252	0.000
30	THYMU2016523	0.000	23.416
	THYMU2023967	0.000	43.363
	THYMU2030264	0.000	45.981
	THYMU2033308	13.964	0.000
	THYMU2035735	1.319	0.936
35	THYMU2039315	54.530	0.000
	THYMU2039780	0.000	45.981

	THYMU3001083	0.000	45.981
	THYMU3001234	11.085	7.868
	THYMU3003309	0.000	20.635
	THYMU3006485	0.000	45.981
5	THYMU3008171	20.170	14.316
	TKIDN2009641	5.782	4.104
	TKIDN2009889	35.077	0.000
	TKIDN2015788	5.261	0.000
	TRACH1000205	19.677	8.380
10	TRACH2001549	8.457	0.000
	TRACH2005811	2.109	0.000
	TRACH2006049	47.167	0.000
	TRACH2007834	0.504	0.000
	TRACH2008300	10.186	3.615
15	TRACH2025535	5.806	2.472
	TRACH3001427	5.571	3.295
	TRACH3002192	4.989	3.541
	TRACH3004721	8.721	4.127
	TRACH3005294	7.428	0.000
20	TRACH3006038	0.000	38.787
	TRACH3006412	0.000	38.787
	TRACH3007479	1.075	0.000
	TRACH3008093	2.449	3.477
	TRACH3009455	47.167	0.000
25	TUTER2000904	0.000	5.944
	UTERU2002410	0.000	0.417
	UTERU2006115	7.837	5.563
	UTERU2007520	0.000	4.761
	UTERU2019706	45.606	0.000
30	UTERU2023039	45.606	0.000
	UTERU2026203	45.606	0.000
	UTERU3000226	0.000	37.308
	UTERU3001572	0.000	2.591
	UTERU3005230	24.419	17.332
35	UTERU3005460	0.000	37.308
	UTERU3005970	0.000	37.308

	UTERU3006308	0.000	37.308
	UTERU3007419	0.000	37.308
	UTERU3007640	45.606	0.000
	UTERU3007913	0.000	12.951
5	UTERU3009871	36.230	0.000
	ADRGL2000042	2.540	7.210
	BLADE2006830	1.681	2.386
	BRACE2002589	0.000	100.000
	BRACE2003609	9.090	6.452
10	BRACE2009318	0.000	100.000
	BRACE2011677	0.000	100.000
	BRACE2029396	0.000	100.000
	BRACE2037299	0.000	100.000
	BRACE2039823	0.000	41.329
15	BRACE2039832	0.000	100.000
	BRACE2043105	0.000	100.000
	BRACE3001058	0.000	100.000
	BRACE3001113	0.000	18.680
	BRACE3003026	0.000	11.590
20	BRACE3003053	0.000	36.360
	BRACE3009127	0.000	100.000
	BRACE3010076	0.000	100.000
	BRACE3015829	0.000	100.000
	BRACE3021148	0.000	100.000
25	BRAMY3004800	38.061	0.000
	BRAWH1000369	100.000	0.000
	BRAWH2006207	12.943	9.187
	BRAWH2006395	12.446	0.000
	BRAWH2008993	49.811	0.000
30	BRAWH2009393	100.000	0.000
	BRAWH2010552	58.488	41.512
	BRAWH3007441	100.000	0.000
	BRAWH3009017	100.000	0.000
	BRCOC2019841	0.000	16.691
35	BRHIP2005271	7.083	0.000
	BRHIP3000017	8.819	0.000

	BRHIP3000240	0.000	67.607
	BRTHA2018443	22.098	0.000
	BRTHA3003000	17.150	0.000
	CTONG2020374	31.081	11.030
5	CTONG2020378	16.140	0.000
	CTONG2024031	2.584	3.669
	FCBBF1000509	3.732	0.000
	FEBRA2001990	18.144	15.453
	FEBRA2006519	11.891	25.320
10	FEBRA2028516	8.007	1.624
	HCHON2000743	6.105	8.667
	IMR322001879	9.638	0.000
	NT2RI2009583	0.224	5.399
	NT2RP8000521	0.000	37.067
15	OCBBF2008144	5.768	4.094
	OCBBF2011669	0.000	36.360
	PERIG2007068	3.086	8.761
	PUAEN2006335	12.682	0.000
	SPLEN2039379	5.792	10.278
20	SYNOV2021953	0.000	6.793
	TESTI2015626	0.000	0.467
	TESTI4001984	60.471	0.000
	TESTI4008058	8.814	0.000
	TESTI4013894	0.000	19.881
25	TESTI4025268	60.471	0.000
	TESTI4032090	60.471	0.000
	THYMU2004284	0.000	4.768
	THYMU2040925	0.000	45.981
	THYMU3000360	39.314	27.904
30	TLIVE2002046	5.445	7.729
	TRACH3000134	36.165	0.000
	UTERU2008040	0.000	8.353
	UTERU2011220	0.000	1.389
	UTERU2021820	24.929	17.694
35	UTERU2028734	21.953	0.000

The result of comparative analysis of cDNA libraries derived from the thalamus (BRTHA), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

5

Table 8

	Clone ID	BRAWH	BRTHA
10	ASTR01000009	2.611	0.000
	ASTR03000482	0.000	24.247
	BLADE2008398	12.401	13.752
	BRACE1000186	4.324	0.000
	BRACE1000258	31.956	0.000
15	BRACE1000533	11.795	5.232
	BRACE2005457	58.488	0.000
	BRACE2010489	63.510	0.000
	BRACE2014306	0.000	5.398
	BRACE2014657	15.451	0.000
20	BRACE2015058	0.000	19.449
	BRACE2031154	0.000	60.975
	BRACE2035381	10.177	11.286
	BRACE2044286	18.667	0.000
	BRACE2045954	27.309	0.000
25	BRACE3000787	32.844	12.141
	BRACE3003192	58.488	0.000
	BRACE3005499	31.276	0.000
	BRACE3007480	19.471	7.197
	BRACE3008384	0.000	43.859
30	BRACE3009237	18.139	20.116
	BRACE3009724	58.488	0.000
	BRACE3009747	2.237	2.481
	BRACE3010397	0.000	75.757
	BRACE3010428	6.868	2.539
35	BRACE3011271	11.036	0.000
	BRACE3011421	28.251	0.000

	BRACE3012364	8. 506	9. 433
	BRACE3022769	4. 285	4. 752
	BRACE3026735	24. 173	0. 000
	BRACE3027478	0. 000	35. 497
5	BRACE3031838	58. 488	0. 000
	BRALZ2011796	5. 511	6. 112
	BRAMY2003008	26. 445	0. 000
	BRAMY2005052	11. 612	25. 755
	BRAMY2019300	49. 811	0. 000
10	BRAMY2019963	20. 428	7. 551
	BRAMY2028914	0. 000	19. 645
	BRAMY2031317	0. 000	34. 791
	BRAMY2036567	7. 474	0. 000
	BRAMY2037823	29. 664	0. 000
15	BRAMY2040592	3. 482	0. 000
	BRAMY2044078	0. 000	19. 449
	BRAMY3002803	14. 428	0. 000
	BRAMY3004224	33. 027	0. 000
	BRAMY3005091	19. 193	0. 000
20	BRAMY4000229	0. 000	39. 237
	BRAWH1000127	15. 983	7. 090
	BRAWH2001395	14. 290	11. 652
	BRAWH2001671	7. 605	12. 650
	BRAWH2001940	37. 398	0. 000
25	BRAWH2001973	37. 398	0. 000
	BRAWH2002560	6. 454	0. 000
	BRAWH2002761	100. 000	0. 000
	BRAWH2005315	100. 000	0. 000
	BRAWH2007658	58. 101	0. 000
30	BRAWH2010000	18. 745	0. 000
	BRAWH2010084	100. 000	0. 000
	BRAWH2010536	14. 718	0. 000
	BRAWH2012162	36. 060	0. 000
	BRAWH2012326	100. 000	0. 000
35	BRAWH2013294	39. 442	0. 000
	BRAWH2013871	37. 485	0. 000

	BRAWH2014414	17.865	9.906
	BRAWH2014645	4.228	1.172
	BRAWH2014662	15.521	17.212
	BRAWH2014876	10.473	58.068
5	BRAWH2014954	58.488	0.000
	BRAWH2016221	47.417	52.583
	BRAWH2016439	100.000	0.000
	BRAWH2016702	73.807	0.000
	BRAWH2016724	35.119	0.000
10	BRAWH3000078	100.000	0.000
	BRAWH3000100	100.000	0.000
	BRAWH3000314	71.553	0.000
	BRAWH3000491	100.000	0.000
	BRAWH3001326	45.606	0.000
15	BRAWH3001475	100.000	0.000
	BRAWH3001891	34.539	0.000
	BRAWH3002574	13.222	0.000
	BRAWH3002600	36.800	0.000
	BRAWH3002819	100.000	0.000
20	BRAWH3002821	21.953	0.000
	BRAWH3003522	100.000	0.000
	BRAWH3003555	15.229	8.444
	BRAWH3003727	10.055	0.000
	BRAWH3003801	100.000	0.000
25	BRAWH3003992	29.008	0.000
	BRAWH3004453	100.000	0.000
	BRAWH3004666	49.499	0.000
	BRAWH3005132	49.811	0.000
	BRAWH3005422	100.000	0.000
30	BRAWH3005912	100.000	0.000
	BRAWH3005981	29.324	0.000
	BRAWH3006548	71.018	0.000
	BRAWH3006792	49.499	0.000
	BRAWH3007221	100.000	0.000
35	BRAWH3007506	100.000	0.000
	BRAWH3007592	8.966	0.000

	BRAWH3007726	54.530	0.000
	BRAWH3007783	100.000	0.000
	BRAWH3008341	100.000	0.000
	BRAWH3008697	100.000	0.000
5	BRAWH3008931	3.463	0.000
	BRAWH3009297	58.488	0.000
	BRCAN2006297	0.000	15.966
	BRCOC2003213	10.381	0.000
	BRCOC2014033	15.633	0.000
10	BRCOC2020142	22.014	0.000
	BRHIP2000819	0.000	4.791
	BRHIP2000920	36.630	0.000
	BRHIP2005719	49.499	0.000
	BRHIP2007741	6.943	5.775
15	BRHIP2009474	0.000	52.083
	BRHIP2013699	0.000	23.663
	BRHIP2014228	29.439	0.000
	BRHIP2022221	0.000	52.083
	BRHIP2024146	3.042	7.759
20	BRHIP3000339	14.290	11.652
	BRHIP3006683	24.100	26.726
	BRHIP3007586	17.255	11.481
	BRHIP3008405	35.187	0.000
	BRHIP3018797	30.810	10.399
25	BRSSN2000684	23.433	10.395
	BRSSN2008549	0.000	18.953
	BRSSN2008797	0.000	22.955
	BRSSN2011738	31.553	0.000
	BRSSN2014299	3.695	0.000
30	BRSTN2004863	0.000	11.049
	BRSTN2008052	32.844	12.141
	BRSTN2015015	14.017	15.544
	BRSTN2016470	0.438	0.000
	BRTHA1000311	11.803	9.817
35	BRTHA2000855	0.000	100.000
	BRTHA2001462	0.000	100.000

	BRTHA2002115	0.000	100.000
	BRTHA2002281	0.000	100.000
	BRTHA2002376	0.000	100.000
	BRTHA2002442	0.000	68.493
5	BRTHA2002493	0.000	100.000
	BRTHA2002608	0.000	100.000
	BRTHA2002808	0.000	12.857
	BRTHA2003030	0.000	100.000
	BRTHA2003110	0.000	100.000
10	BRTHA2003116	0.000	100.000
	BRTHA2003461	0.000	2.434
	BRTHA2004821	0.000	100.000
	BRTHA2004978	0.000	100.000
	BRTHA2005579	0.000	100.000
15	BRTHA2005956	0.000	100.000
	BRTHA2006075	0.000	100.000
	BRTHA2006146	0.000	100.000
	BRTHA2006194	0.000	100.000
	BRTHA2007122	0.000	100.000
20	BRTHA2007422	0.000	100.000
	BRTHA2007603	0.000	100.000
	BRTHA2008316	0.000	100.000
	BRTHA2008335	16.281	9.028
	BRTHA2008527	0.000	100.000
25	BRTHA2008535	0.000	100.000
	BRTHA2008955	0.000	60.975
	BRTHA2009311	0.000	100.000
	BRTHA2009846	0.000	100.000
	BRTHA2009972	0.000	100.000
30	BRTHA2010073	0.000	100.000
	BRTHA2010608	0.000	48.181
	BRTHA2010884	0.000	100.000
	BRTHA2010907	0.000	100.000
	BRTHA2011194	0.000	60.975
35	BRTHA2011351	0.000	100.000
	BRTHA2011500	0.000	100.000

	BRTHA2011641	0.000	52.395
	BRTHA2012392	0.000	38.390
	BRTHA2012562	0.000	100.000
	BRTHA2012980	0.000	13.890
5	BRTHA2013262	0.000	100.000
	BRTHA2013460	0.000	100.000
	BRTHA2013707	0.000	100.000
	BRTHA2014792	0.000	100.000
	BRTHA2014828	0.000	100.000
10	BRTHA2015406	0.000	100.000
	BRTHA2015478	0.000	100.000
	BRTHA2015696	0.000	100.000
	BRTHA2015878	0.000	100.000
	BRTHA2016215	0.000	38.930
15	BRTHA2016496	0.000	100.000
	BRTHA2016543	0.000	100.000
	BRTHA2017353	0.000	100.000
	BRTHA2017985	0.000	49.749
	BRTHA2018165	0.000	100.000
20	BRTHA2018344	0.000	100.000
	BRTHA2018591	0.000	100.000
	BRTHA2018624	0.000	100.000
	BRTHA2018707	0.000	57.080
	BRTHA2019014	0.000	100.000
25	BRTHA2019022	0.000	100.000
	BRTHA2019048	0.000	100.000
	BRTHA3000273	0.000	57.080
	BRTHA3000297	0.000	52.083
	BRTHA3000633	0.000	37.898
30	BRTHA3001721	0.000	13.062
	BRTHA3002401	0.000	100.000
	BRTHA3002427	8.577	15.852
	BRTHA3002933	0.000	100.000
	BRTHA3003074	0.000	37.459
35	BRTHA3003343	0.000	100.000
	BRTHA3003449	0.000	100.000

	BRTHA3003474	0.000	100.000
	BRTHA3003490	1.623	1.800
	BRTHA3004475	0.000	52.395
	BRTHA3005046	0.000	52.083
5	BRTHA3006856	0.000	100.000
	BRTHA3007113	0.000	100.000
	BRTHA3007148	0.000	100.000
	BRTHA3007319	0.000	100.000
	BRTHA3007769	0.000	100.000
10	BRTHA3008143	0.000	100.000
	BRTHA3008310	0.000	100.000
	BRTHA3008386	0.000	100.000
	BRTHA3008520	47.417	52.583
	BRTHA3008778	0.000	27.551
15	BRTHA3009037	0.000	100.000
	BRTHA3009090	0.000	13.052
	BRTHA3009291	0.000	100.000
	BRTHA3010366	0.000	100.000
	BRTHA3013884	0.000	100.000
20	BRTHA3015815	0.000	100.000
	BRTHA3015910	0.000	33.089
	BRTHA3016845	0.000	100.000
	BRTHA3016917	0.000	100.000
	BRTHA3017047	0.000	100.000
25	BRTHA3017589	0.000	100.000
	BRTHA3017848	47.417	52.583
	BRTHA3018514	0.000	100.000
	BRTHA3018617	0.000	100.000
	BRTHA3018656	0.000	100.000
30	BRTHA3019105	0.000	100.000
	COLON2001721	11.065	0.000
	CTONG1000087	0.000	3.479
	CTONG2008233	0.000	3.046
	CTONG2017500	2.649	2.938
35	CTONG2019788	0.000	3.391
	CTONG2023021	0.000	37.320

	CTONG2028124	0.503	1.672
	CTONG3000657	3.880	8.605
	CTONG3001123	7.847	0.000
	CTONG3008894	0.000	2.418
5	CTONG3009028	0.000	1.785
	CTONG3009239	0.000	1.601
	CTONG3009328	11.993	0.000
	FCBBF2001183	16.537	9.169
	FCBBF3001977	7.448	0.000
10	FCBBF3021576	0.000	19.062
	FEBRA2007544	14.689	2.715
	FEBRA2007801	4.937	5.475
	FEBRA2008287	0.000	6.537
	FEBRA2008360	0.000	11.338
15	FEBRA2020886	12.124	0.000
	FEBRA2028618	5.082	0.000
	HCASM2007047	3.431	0.000
	HCHON2000028	0.000	5.278
	HCHON2000212	0.000	19.062
20	HCHON2000244	0.658	0.000
	HCHON2000626	2.351	1.304
	HCHON2001084	0.000	2.546
	HCHON2001217	3.123	5.771
	HCHON2002676	13.647	0.000
25	HCHON2005921	0.000	9.198
	HCHON2006250	1.565	1.735
	HEART1000074	0.759	0.000
	HEART2007031	0.000	12.601
	HHDPC1000118	2.096	0.000
30	HLUNG2001996	0.000	23.216
	HLUNG2002465	1.209	1.341
	IMR322000127	3.098	0.000
	IMR322001300	0.000	2.198
	IMR322002035	36.176	0.000
35	KIDNE2002252	0.000	2.417
	KIDNE2005543	0.000	19.748

	KIDNE2006580	7.013	7.777
	KIDNE2011314	0.000	24.133
	MESAN2006563	0.691	1.532
	MESAN2012054	12.754	0.000
5	MESTC1000042	2.245	0.000
	NOVAR2001783	4.027	0.000
	NT2NE2006909	0.285	0.000
	NT2RI2008724	1.836	4.073
	NT2RI2012659	13.562	0.000
10	NT2RI2014733	24.938	0.000
	NT2RI3002842	0.000	20.781
	NT2RI3002892	8.799	13.661
	NT2RI3005403	0.000	37.898
	NT2RI3006284	4.138	0.000
15	NT2RI3006673	19.959	0.000
	NT2RI3007543	1.697	0.000
	NT2RI3008055	44.179	0.000
	NT2RP7004123	0.000	2.128
	NT2RP7005529	14.766	0.000
20	NT2RP7009147	14.337	3.533
	NT2RP7014005	5.818	0.000
	NT2RP7017474	18.823	0.000
	NTONG2005969	0.000	3.562
	NTONG2008088	0.000	11.332
25	OCBBF2001794	4.728	0.000
	OCBBF2006005	9.535	21.147
	OCBBF2006764	15.345	0.000
	OCBBF2007028	9.665	18.374
	OCBBF2010140	32.508	0.000
30	OCBBF2020639	0.000	25.048
	OCBBF2021286	18.456	10.233
	OCBBF2024719	0.000	32.892
	OCBBF2024850	4.445	7.393
	OCBBF2028935	5.789	2.568
35	OCBBF2036743	11.053	12.257
	OCBBF2038317	19.713	10.930

	OCBBF3000483	11. 973	0. 000
	OCBBF3008230	29. 840	33. 091
	PEBLM2004666	3. 715	0. 000
	PLACE6001185	21. 358	0. 000
5	PUAEN2002489	0. 000	21. 707
	PUAEN2005930	18. 362	10. 181
	PUAEN2006701	2. 249	0. 000
	PUAEN2007044	8. 600	1. 590
	PUAEN2009655	18. 275	0. 000
10	RECTM2001347	0. 000	4. 600
	SKMUS2000757	0. 000	5. 480
	SPLEN2006122	0. 000	0. 934
	SPLEN2010912	0. 000	13. 734
	SPLEN2025491	0. 000	38. 930
15	SPLEN2028914	2. 792	0. 000
	SPLEN2031424	15. 229	8. 444
	SPLEN2031547	1. 574	1. 746
	SPLEN2032154	0. 000	38. 930
	SPLEN2034781	27. 984	0. 000
20	SPLEN2036821	0. 000	38. 930
	SPLEN2036932	2. 932	0. 000
	SYNOV1000374	0. 000	22. 005
	SYNOV2014400	12. 977	0. 000
	SYNOV4002346	5. 997	0. 000
25	SYNOV4002883	23. 940	0. 000
	SYNOV4007430	31. 677	0. 000
	SYNOV4007671	0. 000	0. 813
	SYNOV4008440	1. 475	3. 272
	TESOP2002451	2. 375	0. 000
30	TESTI2049246	0. 000	29. 159
	TESTI4000014	1. 964	1. 188
	TESTI4000209	2. 649	2. 938
	TESTI4001100	4. 098	4. 544
	TESTI4002290	0. 000	62. 915
35	TESTI4006137	25. 755	28. 561
	TESTI4008797	12. 429	27. 567

	TESTI4009286	1.450	0.804
	TESTI4010851	3.280	3.031
	TESTI4012702	0.000	2.417
	TESTI4013817	27.163	0.000
5	TESTI4014159	0.000	25.996
	TESTI4014694	2.229	0.000
	TESTI4021478	22.098	49.012
	TESTI4022936	26.445	0.000
	TESTI4024420	37.398	0.000
10	TESTI4027821	60.471	0.000
	TESTI4037156	0.000	0.307
	THYMU2001090	21.252	47.135
	THYMU2025707	0.000	20.521
	THYMU2032825	0.000	20.620
15	THYMU2033308	13.964	0.000
	THYMU2033787	0.000	57.080
	THYMU2035735	1.319	0.000
	THYMU2039315	54.530	0.000
	THYMU2040975	0.000	1.948
20	THYMU3001234	11.085	12.293
	THYMU3001379	0.000	27.929
	THYMU3004835	0.000	21.784
	THYMU3008171	20.170	0.000
	TKIDN2009641	5.782	12.823
25	TKIDN2009889	35.077	0.000
	TKIDN2015788	5.261	2.917
	TLIVE2001327	0.000	5.201
	TRACH1000205	19.677	0.000
	TRACH2001549	8.457	4.689
30	TRACH2005811	2.109	3.508
	TRACH2006049	47.167	0.000
	TRACH2007834	0.504	0.559
	TRACH200°300	10.1°6	11.296
	TRACH2023299	0.000	14.157
35	TRACH2025535	5.806	1.288
	TRACH3001427	5.571	1.030

	TRACH3002192	4.989	2.766
	TRACH3004068	0.000	1.581
	TRACH3004721	8.721	3.224
	TRACH3005294	7.428	0.000
5	TRACH3007479	1.075	0.000
	TRACH3008093	2.449	2.716
	TRACH3009455	47.167	0.000
	TSTOM1000135	0.000	9.361
	TUTER2000904	0.000	3.096
10	UTERU2002410	0.000	1.302
	UTERU2006115	7.837	17.383
	UTERU2019706	45.606	0.000
	UTERU2019940	0.000	48.181
	UTERU2023039	45.606	0.000
15	UTERU2023175	0.000	1.651
	UTERU2026203	45.606	0.000
	UTERU2030280	0.000	48.181
	UTERU3000899	0.000	31.292
	UTERU3001571	0.000	48.181
20	UTERU3001572	0.000	6.073
	UTERU3004709	0.000	48.181
	UTERU3005230	24.419	0.000
	UTERU3005907	0.000	14.514
	UTERU3007640	45.606	0.000
25	UTERU3009871	36.230	0.000
	ADRGL2000042	2.540	0.000
	BLADE2006830	1.681	0.000
	BRACE2003609	9.090	0.000
	BRAMY3004800	38.061	0.000
30	BRAWH1000369	100.000	0.000
	BRAWH2006207	12.943	0.000
	BRAWH2006395	12.446	0.000
	BRAWH2008993	49.811	0.000
	BRAWH2009393	100.000	0.000
35	BRAWH2010552	58.488	0.000
	BRAWH3007441	100.000	0.000

	BRAWH3009017	100.000	0.000
	BRHIP2005271	7.083	7.855
	BRHIP3000017	8.819	0.000
	BRTHA2002133	0.000	100.000
5	BRTHA2002702	0.000	100.000
	BRTHA2007060	0.000	100.000
	BRTHA2010033	0.000	100.000
	BRTHA2011321	0.000	100.000
	BRTHA2013426	0.000	100.000
10	BRTHA2013610	0.000	100.000
	BRTHA2016318	0.000	100.000
	BRTHA2017364	0.000	100.000
	BRTHA2017972	0.000	37.427
	BRTHA2018011	0.000	100.000
15	BRTHA2018443	22.098	49.012
	BRTHA3000296	0.000	100.000
	BRTHA3003000	17.150	19.019
	BRTHA3008826	0.000	100.000
	CTONG2008721	0.000	37.320
20	CTONG2020374	31.081	0.000
	CTONG2020378	16.140	0.000
	CTONG2024031	2.584	0.000
	FCBBF1000509	3.732	6.208
	FEBRA2001990	18.144	8.048
25	FEBRA2006519	11.891	0.000
	FEBRA2028516	8.007	1.268
	HCHON2000743	6.105	6.771
	HSYRA2005628	0.000	7.437
	IMR322001879	9.638	0.000
30	NT2RI2009583	0.224	1.489
	OCBBF2008144	5.768	3.198
	PERIC2007068	3.086	1.711
	PUAEN2006335	12.682	0.000
	SPLEN2016932	0.000	38.930
35	SPLEN2039379	5.792	3.212
	SYNOV2006620	0.000	33.957

	TESTI4001984	60.471	0.000
	TESTI4008058	8.814	0.000
	TESTI4025268	60.471	0.000
	TESTI4032090	60.471	0.000
5	THYMU3000360	39.314	0.000
	TLIVE2002046	5.445	12.076
	TRACH3000134	36.165	0.000
	UTERU2021820	24.929	27.645
	UTERU2028734	21.953	0.000

The result of comparative analysis of cDNA libraries derived from the amygdale (BRAMY), and from whole tissues of a normal brain (BRAWH) showed following genes whose expression levels differed between the two.

Table 9

Clone ID	BRAWH	BRAMY
ASTR01000009	2.611	0.000
BLADE2008398	12.401	0.000
BRACE1000186	4.324	0.000
BRACE1000258	31.956	0.000
BRACE1000533	11.795	4.754
BRACE2005457	58.488	0.000
BRACE2006319	0.000	3.532
BRACE2010489	63.510	10.665
BRACE2014657	15.451	7.784
BRACE2015058	0.000	8.836
BRACE2027258	0.000	34.044
BRACE2030341	0.000	6.969
BRACE2031389	0.000	30.747
BRACE2035301	10.177	10.254
BRACE2044286	18.667	0.000
BRACE2045954	27.309	0.000
BRACE3000787	32.844	0.000

	BRACE3000973	0.000	13.581
	BRACE3003192	58.488	0.000
	BRACE3005499	31.276	0.000
	BRACE3007480	19.471	6.540
5	BRACE3008036	0.000	18.594
	BRACE3009237	18.139	0.000
	BRACE3009724	58.488	0.000
	BRACE3009747	2.237	0.000
	BRACE3010428	6.868	3.460
10	BRACE3011271	11.036	11.120
	BRACE3011421	28.251	0.000
	BRACE3012364	8.506	0.000
	BRACE3013780	0.000	4.833
	BRACE3022769	4.285	4.318
15	BRACE3026735	24.173	24.356
	BRACE3027478	0.000	16.126
	BRACE3031838	58.488	0.000
	BRALZ2011796	5.511	0.000
	BRAMY2001473	0.000	100.000
20	BRAMY2003008	26.445	26.646
	BRAMY2004771	0.000	100.000
	BRAMY2005052	11.612	46.801
	BRAMY2017528	0.000	100.000
	BRAMY2019300	49.811	50.189
25	BRAMY2019963	20.428	6.861
	BRAMY2019985	0.000	100.000
	BRAMY2020058	0.000	28.146
	BRAMY2020270	0.000	100.000
	BRAMY2021498	0.000	100.000
30	BRAMY2028856	0.000	100.000
	BRAMY2028914	0.000	17.849
	BRAMY2029602	0.000	100.000
	BRAMY2030098	0.000	42.496
	BRAMY2030109	0.000	100.000
35	BRAMY2030702	0.000	100.000
	BRAMY2030703	0.000	100.000

	BRAMY2030799	0.000	100.000
	BRAMY2031317	0.000	15.805
	BRAMY2031377	0.000	100.000
	BRAMY2031442	0.000	100.000
5	BRAMY2032014	0.000	100.000
	BRAMY2032242	0.000	100.000
	BRAMY2032317	0.000	60.652
	BRAMY2033003	0.000	100.000
	BRAMY2033116	0.000	100.000
10	BRAMY2033267	0.000	100.000
	BRAMY2033594	0.000	100.000
	BRAMY2034185	0.000	100.000
	BRAMY2034920	0.000	100.000
	BRAMY2034993	0.000	100.000
15	BRAMY2036387	0.000	13.490
	BRAMY2036396	0.000	100.000
	BRAMY2036567	7.474	22.594
	BRAMY2036699	0.000	100.000
	BRAMY2036913	0.000	100.000
20	BRAMY2037823	29.664	29.890
	BRAMY2038100	0.000	100.000
	BRAMY2038484	0.000	100.000
	BRAMY2038846	0.000	47.355
	BRAMY2038904	0.000	60.652
25	BRAMY2039872	0.000	19.976
	BRAMY2040478	0.000	100.000
	BRAMY2040592	3.482	7.017
	BRAMY2041261	0.000	100.000
	BRAMY2041378	0.000	100.000
30	BRAMY2041542	0.000	100.000
	BRAMY2042612	0.000	100.000
	BRAMY2042641	0.000	100.000
	BRAMY2042760	0.000	100.000
	BRAMY2042918	0.000	100.000
35	BRAMY2044078	0.000	8.836
	BRAMY2044246	0.000	100.000

	BRAMY2045036	0.000	100.000
	BRAMY2046478	0.000	100.000
	BRAMY2046742	0.000	100.000
	BRAMY2046989	0.000	100.000
5	BRAMY2047169	0.000	100.000
	BRAMY2047420	0.000	2.041
	BRAMY2047676	0.000	100.000
	BRAMY2047746	0.000	100.000
	BRAMY2047751	0.000	100.000
10	BRAMY2047765	0.000	100.000
	BRAMY2047884	0.000	100.000
	BRAMY3000206	0.000	100.000
	BRAMY3000213	0.000	100.000
	BRAMY3001401	0.000	100.000
15	BRAMY3001794	0.000	100.000
	BRAMY3002312	0.000	100.000
	BRAMY3002620	0.000	58.671
	BRAMY3002803	14.428	14.538
	BRAMY3002805	0.000	100.000
20	BRAMY3004224	33.027	33.278
	BRAMY3004672	0.000	100.000
	BRAMY3004900	0.000	100.000
	BRAMY3004919	0.000	100.000
	BRAMY3005091	19.193	19.339
25	BRAMY3005932	0.000	58.671
	BRAMY3006297	0.000	100.000
	BRAMY3007206	0.000	100.000
	BRAMY3007609	0.000	100.000
	BRAMY3008466	0.000	100.000
30	BRAMY3008505	0.000	100.000
	BRAMY3008650	0.000	100.000
	BRAMY3009811	0.000	33.057
	BRAMY3010411	0.000	100.000
	BRAMY4000095	0.000	14.721
35	BRAMY4000229	0.000	35.650
	BRAMY4000277	0.000	100.000

	BRAWH1000127	15.983	9.663
	BRAWH2001395	14.290	2.541
	BRAWH2001671	7.605	0.000
	BRAWH2001940	37.398	0.000
5	BRAWH2001973	37.398	0.000
	BRAWH2002560	6.454	6.503
	BRAWH2002761	100.000	0.000
	BRAWH2005315	100.000	0.000
	BRAWH2007658	58.101	0.000
10	BRAWH2010000	18.745	0.000
	BRAWH2010084	100.000	0.000
	BRAWH2010536	14.718	0.000
	BRAWH2012162	36.060	0.000
	BRAWH2012326	100.000	0.000
15	BRAWH2013294	39.442	0.000
	BRAWH2013871	37.485	0.000
	BRAWH2014414	17.865	54.002
	BRAWH2014645	4.228	2.130
	BRAWH2014662	15.521	0.000
20	BRAWH2014876	10.473	0.000
	BRAWH2014954	58.488	0.000
	BRAWH2016221	47.417	0.000
	BRAWH2016439	100.000	0.000
	BRAWH2016702	73.807	0.000
25	BRAWH2016724	35.119	0.000
	BRAWH3000078	100.000	0.000
	BRAWH3000100	100.000	0.000
	BRAWH3000314	71.553	0.000
	BRAWH3000491	100.000	0.000
30	BRAWH3001326	45.606	0.000
	BRAWH3001475	100.000	0.000
	BRAWH3001891	34.539	17.401
	BRAWH3002574	13.222	0.000
	BRAWH3002600	36.800	37.080
35	BRAWH3002819	100.000	0.000
	BRAWH3002821	21.953	0.000

	BRAWH3003522	100.000	0.000
	BRAWH3003555	15.229	0.000
	BRAWH3003727	10.055	0.000
	BRAWH3003801	100.000	0.000
5	BRAWH3003992	29.008	0.000
	BRAWH3004453	100.000	0.000
	BRAWH3004666	49.499	0.000
	BRAWH3005132	49.811	50.189
	BRAWH3005422	100.000	0.000
10	BRAWH3005912	100.000	0.000
	BRAWH3005981	29.324	0.000
	BRAWH3006548	71.018	0.000
	BRAWH3006792	49.499	0.000
	BRAWH3007221	100.000	0.000
15	BRAWH3007506	100.000	0.000
	BRAWH3007592	8.966	1.807
	BRAWH3007726	54.530	0.000
	BRAWH3007783	100.000	0.000
	BRAWH3008341	100.000	0.000
20	BRAWH3008697	100.000	0.000
	BRAWH3008931	3.463	6.980
	BRAWH3009297	58.488	0.000
	BRCAN2014881	0.000	30.516
	BRCAN2017717	0.000	10.719
25	BRCOC2000670	0.000	22.144
	BRCOC2003213	10.381	0.000
	BRCOC2014033	15.633	0.000
	BRCOC2020142	22.014	0.000
	BRHIP2000920	36.630	0.000
30	BRHIP2005719	49.499	0.000
	BRHIP2007741	6.943	8.745
	BRHIP2014228	29.439	0.000
	BRHIP2024146	3.042	2.759
	BRHIP2026061	0.000	30.812
35	BRHIP3000339	14.290	2.541
	BRHIP3001283	0.000	49.688

	BRHIP3006683	24.100	0.000
	BRHIP3007586	17.255	3.477
	BRHIP3008405	35.187	0.000
	BRHIP3018797	30.810	9.448
5	BRSSN2000684	23.433	0.000
	BRSSN2004496	0.000	21.304
	BRSSN2011738	31.553	0.000
	BRSSN2014299	3.695	0.000
	BRSTN2008052	32.844	0.000
10	BRSTN2010750	0.000	30.747
	BRSTN2015015	14.017	0.000
	BRSTN2016470	0.438	0.441
	BRTHA1000311	11.803	14.866
	BRTHA2008335	16.281	0.000
15	BRTHA2011641	0.000	47.605
	BRTHA3001721	0.000	23.737
	BRTHA3002427	8.577	5.761
	BRTHA3003490	1.623	0.000
	BRTHA3004475	0.000	47.605
20	BRTHA3008520	47.417	0.000
	BRTHA3009090	0.000	11.859
	BRTHA3017848	47.417	0.000
	COLON2001721	11.065	11.149
	CTONG1000087	0.000	3.161
25	CTONG2008233	0.000	0.692
	CTONG2017500	2.649	2.669
	CTONG2028124	0.503	0.506
	CTONG3000657	3.880	0.000
	CTONG3001123	7.847	0.000
30	CTONG3008894	0.000	4.395
	CTONG3009239	0.000	4.364
	CTONG3009328	11.993	0.000
	FCBBF20011^3	16.537	9.998
	FCBBF3001977	7.448	15.010
35	FEBRA2007544	14.689	0.000
	FEBRA2007801	4.937	0.000

	FEBRA2008287	0.000	2.970
	FEBRA2010719	0.000	17.484
	FEBRA2020886	12.124	0.000
	FEBRA2025427	0.000	4.995
5	FEBRA2028618	5.082	5.121
	HCASM2007047	3.431	0.000
	HCHON2000244	0.658	0.663
	HCHON2000626	2.351	0.000
	HCHON2001217	3.123	0.000
10	HCHON2002676	13.647	0.000
	HCHON2006250	1.565	0.000
	HCHON2008112	0.000	13.736
	HEART1000074	0.759	0.000
	HHDPC1000118	2.096	0.000
15	HLUNG2002465	1.209	4.875
	HSYRA2009075	0.000	1.212
	IMR322000127	3.098	10.926
	IMR322001380	0.000	11.984
	IMR322002035	36.176	0.000
20	KIDNE2000665	0.000	1.951
	KIDNE2006580	7.013	7.066
	MESAN2006563	0.691	0.000
	MESAN2012054	12.754	0.000
	MESAN2015515	0.000	2.677
25	MESTC1000042	2.245	0.000
	NOVAR2001783	4.027	0.000
	NT2NE2005890	0.000	35.735
	NT2NE2006909	0.285	0.287
	NT2RI2008724	1.836	1.850
30	NT2RI2012659	13.562	13.665
	NT2RI2014733	24.938	0.000
	NT2RI3001515	0.000	21.825
	NT2RI3002^92	8.799	1.773
	NT2RI3005724	0.000	5.972
35	NT2RI3006284	4.138	0.000
	NT2RI3006673	19.959	10.055

	NT2RI3007543	1.697	0.855
	NT2RI3008055	44.179	0.000
	NT2RP7005529	14.766	7.439
	NT2RP7009147	14.337	0.000
5	NT2RP7014005	5.818	0.000
	NT2RP7017474	18.823	0.000
	NTONG2005969	0.000	6.473
	OCBBF1000254	0.000	44.784
	OCBBF2001794	4.728	4.764
10	OCBBF2006005	9.535	0.000
	OCBBF2006764	15.345	15.461
	OCBBF2007028	9.665	6.956
	OCBBF2007114	0.000	21.540
	OCBBF2010140	32.508	0.000
15	OCBBF2021286	18.456	0.000
	OCBBF2023162	0.000	31.080
	OCBBF2024850	4.445	2.239
	OCBBF2028935	5.789	1.167
	OCBBF2035214	0.000	44.784
20	OCBBF2036743	11.053	11.137
	OCBBF2038317	19.713	0.000
	OCBBF3000483	11.973	4.021
	OCBBF3008230	29.840	0.000
	PEBLM2004666	3.715	3.744
25	PERIC2000889	0.000	8.963
	PERIC2003720	0.000	13.012
	PLACE6001185	21.358	0.000
	PUAEN2005930	18.362	0.000
	PUAEN2006701	2.249	0.000
30	PUAEN2007044	8.600	1.444
	PUAEN2009174	0.000	2.856
	PUAEN2009655	18.275	0.000
	SKNMC2002402	0.000	7.428
	SKNSH2000482	0.000	9.821
35	SPLEN2001599	0.000	7.190
	SPLEN2002467	0.000	6.565

	SPLEN2028914	2.792	0.000
	SPLEN2029912	0.000	1.646
	SPLEN2031424	15.229	0.000
	SPLEN2031547	1.574	4.759
5	SPLEN2034781	27.984	0.000
	SPLEN2036932	2.932	0.000
	SPLEN2038345	0.000	29.627
	SYNOV2014400	12.977	0.000
	SYNOV4002346	5.997	0.000
10	SYNOV4002883	23.940	0.000
	SYNOV4007430	31.677	0.000
	SYNOV4007671	0.000	0.739
	SYNOV4008440	1.475	0.000
	TESOP2002451	2.375	0.000
15	TESTI2009474	0.000	2.036
	TESTI4000014	1.964	1.799
	TESTI4000209	2.649	2.669
	TESTI4001100	4.098	4.129
	TESTI4006137	25.755	0.000
20	TESTI4008797	12.429	0.000
	TESTI4009286	1.450	0.000
	TESTI4010851	3.280	2.203
	TESTI4013817	27.163	27.369
	TESTI4014159	0.000	11.810
25	TESTI4014694	2.229	0.000
	TESTI4021478	22.098	0.000
	TESTI4022936	26.445	26.646
	TESTI4024420	37.398	0.000
	TESTI4027821	60.471	0.000
30	TESTI4029836	0.000	60.652
	TESTI4037156	0.000	1.394
	TESTI4037188	0.000	60.652
	THYMU2001090	21.252	0.000
	THYMU2014353	0.000	37.663
35	THYMU2033308	13.964	0.000
	THYMU2035735	1.319	0.000

	THYMU2037226	0.000	17.265
	THYMU2039315	54.530	0.000
	THYMU3001234	11.085	0.000
	THYMU3001379	0.000	25.376
5	THYMU3004835	0.000	19.793
	THYMU3008171	20.170	0.000
	TKIDN2009641	5.782	5.826
	TKIDN2009889	35.077	0.000
	TKIDN2015788	5.261	5.301
10	TLIVE2004320	0.000	12.783
	TRACH1000205	19.677	3.965
	TRACH2001549	8.457	4.260
	TRACH2001684	0.000	17.948
	TRACH2005811	2.109	0.000
15	TRACH2006049	47.167	0.000
	TRACH2007834	0.504	1.016
	TRACH2008300	10.186	11.974
	TRACH2025344	0.000	19.846
	TRACH2025535	5.806	0.000
20	TRACH2025911	0.000	47.355
	TRACH3001427	5.571	3.742
	TRACH3002192	4.989	1.885
	TRACH3004068	0.000	1.436
	TRACH3004721	8.721	5.858
25	TRACH3005294	7.428	0.000
	TRACH3007479	1.075	1.084
	TRACH3008093	2.449	0.000
	TRACH3009455	47.167	0.000
	TUTER2000904	0.000	2.813
30	UTERU2002410	0.000	0.592
	UTERU2004929	0.000	11.697
	UTERU2006115	7.837	0.000
	UTERU2007520	0.000	6.758
	UTERU2019706	45.606	0.000
35	UTERU2023039	45.606	0.000
	UTERU2026203	45.606	0.000

	UTERU3001572	0.000	1.839
	UTERU3001766	0.000	45.794
	UTERU3005230	24.419	0.000
	UTERU3007640	45.606	0.000
5	UTERU3009517	0.000	45.794
	UTERU3009871	36.230	0.000
	ADRG2000042	2.540	5.118
	BLADE2006830	1.681	0.000
	BRACE2003609	9.090	18.317
10	BRACE2039823	0.000	58.671
	BRAMY2019111	0.000	30.516
	BRAMY2035070	0.000	54.718
	BRAMY2035449	0.000	100.000
	BRAMY2035718	0.000	100.000
15	BRAMY2038516	0.000	12.770
	BRAMY2039341	0.000	100.000
	BRAMY2040159	0.000	100.000
	BRAMY2041434	0.000	100.000
	BRAMY2045471	0.000	100.000
20	BRAMY3004800	38.061	15.340
	BRAWH1000369	100.000	0.000
	BRAWH2006207	12.943	0.000
	BRAWH2006395	12.446	0.000
	BRAWH2008993	49.811	50.189
25	BRAWH2009393	100.000	0.000
	BRAWH2010552	58.488	0.000
	BRAWH3007441	100.000	0.000
	BRAWH3009017	100.000	0.000
	BRHIP2005271	7.083	7.137
30	BRHIP3000017	8.819	0.000
	BRTHA2018443	22.098	0.000
	BRTHA3003000	17.150	0.000
	CTONG2020374	31.081	0.000
	CTONG2020378	16.140	0.000
35	CTONG2024031	2.584	0.000
	FCBBF1000509	3.732	13.160

	FEBRA2001990	18.144	7.313
	FEBRA2006519	11.891	11.982
	FEBRA2028516	8.007	2.305
	HCHON2000508	0.000	0.376
5	HCHON2000743	6.105	0.000
	IMR322001879	9.638	0.000
	NT2RI2009583	0.224	0.902
	OCBBF2008144	5.768	2.906
	PERIC2007068	3.086	0.000
10	PUAEN2006335	12.682	0.000
	SPLEN2039379	5.792	11.672
	TESTI2015626	0.000	0.331
	TESTI2026647	0.000	23.811
	TESTI4001984	60.471	0.000
15	TESTI4008058	8.814	0.000
	TESTI4013894	0.000	14.112
	TESTI4025268	60.471	0.000
	TESTI4032090	60.471	0.000
	THYMU3000360	39.314	0.000
20	TKIDN2018926	0.000	21.396
	TLIVE2002046	5.445	10.972
	TRACH3000134	36.165	0.000
	UTERU2008040	0.000	11.858
	UTERU2021820	24.929	0.000
25	UTERU2028734	21.953	0.000

The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES), and normal breast (BEAST) showed the following genes whose expression levels differed between the two.

Table 10

Clone ID	BEAST	TBAES
ASTRO2002842	0.000	67.001

	BRACE3016884	0.000	90.835
	BRSSN2011262	61.476	0.000
	BRTHA2008335	0.000	57.267
	HCHON2000244	0.000	4.627
5	HCHON2006250	0.000	11.007
	HEART1000010	0.000	24.034
	MESAN2012054	0.000	35.889
	NT2RP7000466	0.000	85.728
	NT2RP7009147	0.000	11.206
10	OCBBF2021020	0.000	18.756
	PEBLM2002749	0.000	48.344
	PEBLM2004666	0.000	26.137
	SPLEN2001599	0.000	50.196
	SPLEN2031547	0.000	11.076
15	STOMA1000189	0.000	22.002
	TBAES2001171	0.000	100.000
	TBAES2001220	0.000	100.000
	TBAES2001229	0.000	100.000
	TBAES2001258	0.000	66.863
20	TBAES2001492	0.000	100.000
	TBAES2001751	0.000	100.000
	TBAES2002197	0.000	54.528
	TBAES2003550	0.000	100.000
	TBAES2004055	0.000	100.000
25	TBAES2005157	0.000	100.000
	TBAES2005543	0.000	100.000
	TBAES2006568	0.000	100.000
	TBAES2007964	0.000	100.000
	TESTI4000014	0.000	1.256
30	TESTI4037156	0.000	3.893
	TRACH3002192	0.000	4.387
	TRACH3004068	0.000	10.026
	TSTOM2000553	0.000	11.859
	UTERU2002410	0.000	8.261
35	BRAWH2006395	0.000	87.554
	NT2RI2009583	4.881	0.000

STOMA2004893	0.000	50.829
TBAES2000932	0.000	100.000

5 The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX), and normal cervical duct (CERVX) showed the following genes whose expression levels differed between the two.

Table 11

10	Clone ID	CERVX	TCERX
	BLADE2007666	70.405	0.000
	BRAMY2047420	0.000	21.378
15	BRCAN2007409	0.000	63.318
	BRSTN2016470	0.000	9.238
	CERVX1000042	100.000	0.000
	CERVX2002006	100.000	0.000
	MESAN2006563	14.270	0.000
20	PROST2018090	44.955	0.000
	TCERX2000613	0.000	85.503
	TEST14037156	0.000	5.840
	THYMU2031341	71.304	0.000
	UTERU2004688	22.977	70.393
25	CERVX2002013	100.000	0.000
	NT2RI2009583	0.000	9.443

30 The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN), and normal colon (COLON) showed the following genes whose expression levels differed between the two.

Table 12

35	Clone ID	COLON	TCOLN
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	BRACE3015027	0.000	55.019
	BRAMY2040592	24.447	0.000
	BRSTN2016470	6.147	9.281
	COLON1000030	100.000	0.000
5	COLON2000470	50.006	0.000
	COLON2000568	100.000	0.000
	COLON2001721	38.840	0.000
	COLON2002443	31.658	0.000
	COLON2002520	100.000	0.000
10	COLON2003043	100.000	0.000
	COLON2004478	100.000	0.000
	COLON2005126	100.000	0.000
	COLON2005772	100.000	0.000
	COLON2006282	100.000	0.000
15	COLON2009499	100.000	0.000
	OCBBF2028935	8.128	0.000
	PLACE7000514	33.393	0.000
	RECTM2000433	24.395	0.000
	SYNOV4007671	5.146	0.000
20	TCOLN2002278	0.000	100.000
	TEST12052693	23.507	35.495
	TEST14037156	1.943	0.000
	THYMU2031368	0.000	96.216
	TRACH2025535	16.304	0.000
25	CTONG1000113	79.033	0.000
	NT2RI2009583	0.000	4.744
	NT2RI2018448	44.206	0.000
	TEST12015626	2.309	0.000

30 The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP), and normal esophagus (NESOP) showed the following genes whose expression levels differed between the two.

35 Table 13

	Clone ID	NESOP	TESOP
	BRACE2030341	0.000	47.323
	BRAMY2047420	21.553	0.000
5	BRHIP2003917	0.000	80.343
	BRTHA2003461	0.000	15.017
	CTONG2013178	0.000	64.748
	D30ST3000169	0.000	6.696
	FEBRA2025427	0.000	16.960
10	HCHON2000244	0.000	4.501
	HHDPC1000118	0.000	14.339
	NESOP2000744	100.000	0.000
	NESOP2001433	100.000	0.000
	NESOP2001656	85.181	0.000
15	NESOP2001694	100.000	0.000
	NESOP2001752	96.772	0.000
	NESOP2002738	100.000	0.000
	NT2RI3006284	0.000	14.156
	NT2RP7009147	33.894	0.000
20	PLACE6019932	92.281	0.000
	SYNOV2005216	0.000	66.809
	TESOP1000127	0.000	65.101
	TESOP2000801	0.000	100.000
	TESOP2001122	0.000	100.000
25	TESOP2001166	0.000	100.000
	TESOP2001345	0.000	100.000
	TESOP2001605	0.000	66.809
	TESOP2001818	0.000	100.000
	TESOP2001849	0.000	100.000
30	TESOP2001865	0.000	100.000
	TESOP2001953	0.000	89.137
	TESOP2002273	0.000	27.770
	TESOP2002451	0.000	16.251
	TESOP2002489	0.000	100.000
35	TESOP2002539	0.000	100.000
	TESOP2002950	0.000	90.601

	TESOP2003273	0.000	100.000
	TESOP2003753	0.000	100.000
	TESOP2004114	0.000	100.000
	TESOP2005285	0.000	100.000
5	TESOP2005485	0.000	100.000
	TESOP2005579	0.000	100.000
	TESOP2006041	0.000	100.000
	TESOP2006060	0.000	100.000
	TESOP2006068	0.000	100.000
10	TESOP2006670	0.000	79.728
	TESOP2006746	0.000	100.000
	TESOP2007052	0.000	100.000
	TESOP2007262	0.000	100.000
	TESOP2007636	0.000	100.000
15	TESOP2007688	0.000	100.000
	TESOP2009121	0.000	100.000
	TESOP2009555	0.000	100.000
	TEST14009286	15.424	9.920
	TEST14010851	0.000	3.740
20	THYMU2040975	0.000	12.019
	TRACH2005811	0.000	14.431
	UTERU2023175	0.000	10.186
	CTONG2016942	0.000	78.602
	NT2R12009583	0.000	1.531
25	TESOP2000390	0.000	100.000
	TESOP2001796	0.000	100.000
	TESOP2005199	0.000	100.000
	TESOP2006398	0.000	100.000
	TESOP2006865	0.000	100.000
30	TESOP2007384	0.000	13.734
	TEST12015626	0.000	2.250
	TRACH2000862	0.000	39.606

35 The result of comparative analysis of cDNA libraries
 derived from kidney tumor (TKIDN), and normal kidney (KIDNE)

showed the following genes whose expression levels differed between the two.

Table 14

5			
	Clone ID	KIDNE	TKIDN
	ASTR02018373	0.000	51.654
	BRACE1000186	0.000	16.007
10	BRACE2014306	0.000	18.017
	BRACE2015058	0.000	16.230
	BRACE2016981	0.000	83.911
	BRACE2043665	83.085	0.000
	BRACE3008036	0.000	68.309
15	BRACE3010428	3.991	0.000
	BRACE3022769	0.000	5.287
	BRAMY2019963	0.000	25.206
	BRAMY2044078	0.000	16.230
	BRAWH1000127	0.000	11.833
20	BRAWH2001395	0.000	9.335
	BRAWH2001671	0.000	14.075
	BRAWH2013294	0.000	36.500
	BRAWH2014645	0.000	3.913
	BRHIP2024146	0.000	7.882
25	BRHIP3000339	0.000	9.335
	BRSSN2000684	0.000	17.348
	BRSSN2004719	0.000	19.395
	BRSSN2018581	0.000	49.863
	BRSTN2016470	0.763	0.810
30	BRTHA1000311	0.000	10.923
	BRTHA3002427	0.000	10.582
	CTONG1000087	3.646	0.000
	CTONG2028124	3.504	0.000
	CTONG3000657	0.000	14.362
35	CTONG3008894	2.534	0.000
	FCBBF2001183	0.000	12.243

	FEBRA2008287	0.000	10.911
	HCASM2001301	0.000	35.796
	HCHON2000028	0.000	5.873
	HCHON2000244	4.587	0.000
5	HEART1000074	2.646	0.000
	HHDPC1000118	7.307	0.000
	HSYRA2008376	0.000	5.788
	KIDNE1000064	100.000	0.000
	KIDNE2000665	13.498	0.000
10	KIDNE2000722	100.000	0.000
	KIDNE2000832	32.592	0.000
	KIDNE2000846	100.000	0.000
	KIDNE2001361	80.699	0.000
	KIDNE2001847	12.687	0.000
15	KIDNE2002252	7.600	0.000
	KIDNE2002991	100.000	0.000
	KIDNE2003837	100.000	0.000
	KIDNE2005543	62.084	0.000
	KIDNE2006580	48.900	0.000
20	KIDNE2010264	100.000	0.000
	KIDNE2011314	75.867	0.000
	KIDNE2011532	100.000	0.000
	KIDNE2011635	48.502	51.498
	KIDNE2012945	48.732	0.000
25	KIDNE2013095	100.000	0.000
	NESOP2001656	0.000	14.819
	NTONG2005969	0.000	11.891
	PEBLM2004666	12.953	0.000
	SKMUS2000757	0.000	18.292
30	STOMA1000189	16.356	0.000
	SYNOV4007671	2.556	5.427
	TBAES2001258	33.137	0.000
	TESTI4000014	1.245	0.000
	TESTI4001100	0.000	15.168
35	TESTI4012702	7.600	0.000
	TESTI4046819	0.000	73.082

	THYMU2032014	57.532	0.000
	TKIDN2000701	0.000	84.991
	TKIDN2002424	0.000	100.000
	TKIDN2002632	0.000	100.000
5	TKIDN2003044	0.000	100.000
	TKIDN2004386	0.000	100.000
	TKIDN2005934	0.000	100.000
	TKIDN2005947	0.000	100.000
	TKIDN2006525	0.000	100.000
10	TKIDN2006852	0.000	100.000
	TKIDN2007667	0.000	100.000
	TKIDN2009092	0.000	100.000
	TKIDN2009641	0.000	21.402
	TKIDN2009889	0.000	64.923
15	TKIDN2010934	0.000	74.873
	TKIDN2012824	0.000	100.000
	TKIDN2013287	0.000	64.067
	TKIDN2014757	0.000	100.000
	TKIDN2014771	0.000	100.000
20	TKIDN2015263	0.000	100.000
	TKIDN2015788	0.000	9.737
	TKIDN2016309	0.000	100.000
	TKIDN2019116	0.000	100.000
	TRACH2001443	0.000	34.396
25	TRACH2001684	62.100	0.000
	TRACH2007834	1.758	3.734
	TRACH2008300	0.000	6.284
	TRACH3001427	0.000	3.437
	UTERU2002410	0.000	2.173
30	UTERU2023175	5.190	0.000
	UTERU3001572	0.000	6.758
	BLADE2006830	0.000	6.222
	BRALZ2017844	0.000	50.604
	CTONG2028758	0.000	59.532
35	FCBBF1000509	0.000	6.907
	FEBRA2001990	0.000	13.433

	FEBRA2028516	0.000	4.234
	HCHON2000508	0.000	1.382
	MESAN2005303	0.000	29.326
	NT2RI2009583	10.920	0.828
5	TESTI2015626	0.000	4.869
	TKIDN2008778	0.000	100.000
	TKIDN2012771	0.000	100.000
	TKIDN2018926	0.000	78.604

10 The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE), and normal liver (LIVER) showed the following genes whose expression levels differed between the two.

15 Table 15

	Clone ID	LIVER	TLIVE
	BRCAN2018935	79.072	0.000
20	BRSTN2016470	1.897	0.000
	BRTHA2012980	0.000	86.110
	BRTHA3002427	0.000	19.655
	CTONG2028124	0.000	3.455
	LIVER2007415	100.000	0.000
25	NT2RI2008724	0.000	12.626
	SPLEN2012624	43.831	0.000
	SPLEN2033098	0.000	34.211
	TESOP2002451	0.000	16.330
	TLIVE2000023	0.000	100.000
30	TLIVE2001327	0.000	64.491
	TLIVE2001828	0.000	89.183
	TLIVE2001927	0.000	100.000
	TLIVE2002336	0.000	100.000
	TLIVE2002338	0.000	100.000
35	TLIVE2002690	0.000	41.431
	TLIVE2003197	0.000	100.000

	TLIVE2003225	0.000	100.000
	TLIVE2003381	0.000	100.000
	TLIVE2003970	0.000	15.901
	TLIVE2004110	0.000	70.982
5	TLIVE2004320	0.000	87.217
	TLIVE2004601	0.000	100.000
	TLIVE2005180	0.000	100.000
	TLIVE2006236	0.000	100.000
	TLIVE2006529	0.000	100.000
10	TLIVE2007132	0.000	100.000
	TLIVE2007528	0.000	100.000
	TLIVE2007816	0.000	100.000
	TLIVE2008083	0.000	100.000
	TLIVE2008229	0.000	91.317
15	TLIVE2009541	0.000	100.000
	UTERU2002410	0.000	4.037
	UTERU2005621	19.540	0.000
	LIVER2000247	100.000	0.000
	NT2R12009583	1.939	4.615
20	TEST12015626	0.000	2.261
	TLIVE2001684	0.000	100.000
	TLIVE2002046	0.000	12.478
	TLIVE2007607	0.000	100.000

25 The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG), and normal lung (HLUNG) showed the following genes whose expression levels differed between the two.

30 Table 16

	Clone ID	HLUNG	TLUNG
	BRCAN2021028	38.589	0.000
35	BRHIP2000819	7.923	0.000
	BRSTN2016470	0.803	0.000

	CTONG1000087	3.835	0.000
	CTONG2028124	9.217	0.000
	HCHON2006250	0.000	32.381
	HEART1000074	2.784	0.000
5	HLUNG1000017	100.000	0.000
	HLUNG2000014	100.000	0.000
	HLUNG2001996	76.784	0.000
	HLUNG2002465	4.436	0.000
	HLUNG2002958	100.000	0.000
10	HLUNG2003003	29.311	0.000
	HLUNG2003872	100.000	0.000
	HLUNG2010464	100.000	0.000
	HLUNG2011041	100.000	0.000
	HLUNG2011298	35.254	0.000
15	HLUNG2012049	100.000	0.000
	HLUNG2012287	100.000	0.000
	HLUNG2012727	100.000	0.000
	HLUNG2013204	100.000	0.000
	HLUNG2013304	100.000	0.000
20	HLUNG2013622	100.000	0.000
	HLUNG2013851	100.000	0.000
	HLUNG2014262	100.000	0.000
	HLUNG2014288	100.000	0.000
	HLUNG2014449	100.000	0.000
25	HLUNG2015617	100.000	0.000
	HLUNG2017350	100.000	0.000
	HLUNG2017546	12.944	0.000
	HLUNG2017806	100.000	0.000
	HLUNG2019058	100.000	0.000
30	HSYRA2008376	11.470	0.000
	KIDNE2012945	51.268	0.000
	NT2RI2003993	13.924	0.000
	NT2RP7013795	0.000	89.568
	OCBBF3000483	14.638	0.000
35	SPLEN2028914	10.242	0.000
	SPLEN2031547	5.775	0.000

	SYNOV4007671	2.689	0.000
	TESOP1000127	34.899	0.000
	TESTI2003573	27.394	0.000
	TESTI4000014	0.655	0.000
5	TESTI4037156	2.030	0.000
	TRACH2005811	3.868	0.000
	TRACH3004068	5.227	0.000
	UTERU2005621	8.268	0.000
	FEBRA2028516	4.195	0.000
10	HCHON2000508	1.370	0.000
	HLUNG2013350	100.000	0.000
	HLUNG2015418	76.605	0.000
	HLUNG2015548	100.000	0.000
	HLUNG2016862	100.000	0.000
15	NT2RI2009583	0.000	13.890
	TESTI2015626	2.412	0.000
	TRACH2019672	76.605	0.000

The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER), and normal ovary (NOVER) showed the following genes whose expression levels differed between the two.

Table 17A

Clone ID	NOVAR	TOVAR
CTONG2019788	72.878	0.000
FEBRA2014213	0.000	85.773
30 HLUNG2017546	84.114	0.000
NOVAR2000136	100.000	0.000
NOVAR2000710	83.961	0.000
NOVAR2000962	100.000	0.000
NOVAR2001108	100.000	0.000
35 NOVAR2001783	95.973	0.000
OCBBF3007516	90.145	0.000

	TEST12052693	39.903	0.000
	TOVAR2000649	0.000	100.000
	TOVAR2001281	0.000	100.000
	TOVAR2001730	0.000	100.000
5	TOVAR2002247	0.000	100.000
	TOVAR2002549	0.000	100.000
	TRACH3004068	0.000	31.044

10 The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER), and normal ovary (NOVER) showed the following genes whose expression levels differed between the two.

Table 17B

15	Clone ID	NOVAR	TOVAR
	TEST12015626	7.838	7.163

20 The gene has no different expression levels between normal and diseased ovary. However, the gene showed significantly different expression level in both ovary tumor and normal ovary, compared with other tissues (as in Example 9). Thus, the gene are ovary-specific gene and can be used as diagnostic marker
25 because its association with the disease.

The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed the following genes whose expression levels differed between the two.

30

Table 18

	Clone ID	STOMA	TSTOM
35	BRACE2024627	83.309	0.000
	BRAWH2014645	0.000	22.702

	BRCAN2028355	0.000	31.728
	BRHIP2000819	14.701	46.392
	BRSTN2016470	1.490	0.000
	BRTHA3003490	0.000	34.864
5	COLON2002443	30.687	0.000
	HEART1000010	23.250	0.000
	HLUNG2002465	8.231	0.000
	KIDNE2001847	0.000	78.156
	NT2RP7000466	5.924	0.000
10	PUAEN2006328	0.000	79.193
	SMINT2001818	12.758	0.000
	STOMA1000189	10.642	0.000
	STOMA2003444	91.236	0.000
	STOMA2004294	100.000	0.000
15	STOMA2004925	85.088	0.000
	STOMA2008546	100.000	0.000
	SYNOV4007671	4.989	0.000
	TESTI4000014	0.000	3.835
	TESTI4010851	3.720	0.000
20	THYMU2035735	0.000	28.332
	TRACH2001549	28.775	0.000
	TRACH2005811	0.000	22.648
	TRACH2025535	0.000	12.468
	TSTOM1000135	0.000	90.639
25	TSTOM2000442	0.000	100.000
	TSTOM2000553	0.000	36.203
	TSTOM2002672	0.000	100.000
	UTERU2006115	53.335	0.000
	UTERU3001572	12.423	0.000
30	FEBRA2008692	0.000	52.692
	NT2RI2009583	7.613	0.000
	STOMA2003158	41.655	0.000
	STOMA2004893	49.171	0.000
	TESTI2015626	2.238	0.000

The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed the following genes whose expression levels differed between the two.

5

Table 19

	Clone ID	UTERU	TUTER
10	BNGH42007788	3.672	0.000
	BRACE1000186	2.579	0.000
	BRACE2030341	16.499	0.000
	BRACE3008772	62.692	0.000
	BRACE3009747	2.668	0.000
15	BRACE3010428	5.461	0.000
	BRACE3027478	19.089	0.000
	BRALZ2017359	24.816	0.000
	BRAWH2014645	2.522	0.000
	BRAWH3000314	28.447	0.000
20	BRAWH3001326	54.394	0.000
	BRAWH3002574	7.885	0.000
	BRAWH3002821	26.183	0.000
	BRAWH3003727	11.993	0.000
	BRAWH3007592	4.277	0.000
25	BRCAN2009432	3.141	29.345
	BRCAN2028355	1.762	0.000
	BRHIP3007586	4.116	0.000
	BRHIP3008344	53.896	0.000
	BRHIP3008565	53.896	0.000
30	BRSSN2006892	18.468	0.000
	BRSTN2001067	7.384	0.000
	BRSTN2016470	0.522	0.000
	BRTHA2010608	51.819	0.000
	BRTHA3003074	13.429	0.000
35	CTONG1000087	2.494	0.000
	CTONG1000467	10.248	0.000

	CTONG2028124	2.997	0.000
	CTONG3001123	9.359	0.000
	CTONG3008894	0.867	0.000
	CTONG3009028	3.839	0.000
5	CTONG3009239	1.722	0.000
	FCBBF3004847	39.231	0.000
	FEBRA2026984	20.914	0.000
	FEBRA2028618	6.061	0.000
	HCHON2000244	1.569	0.000
10	HCHON2000418	15.860	0.000
	HCHON2000626	5.608	0.000
	HCHON2001084	2.739	0.000
	HCHON2001217	4.966	0.000
	HCHON2005921	24.732	0.000
15	HCHON2006250	0.000	34.872
	HCHON2008444	15.860	0.000
	HLUNG2003003	28.594	0.000
	HSYRA2008376	1.865	0.000
	KIDNE2002252	2.600	0.000
20	MESAN2014295	24.337	0.000
	NOVAR2000710	4.201	0.000
	NT2RI2008724	2.190	0.000
	NT2RI2014247	18.191	0.000
	NT2RI2014733	29.743	0.000
25	NT2RI3002892	18.890	0.000
	NT2RI3005724	7.069	0.000
	NT2RI3006284	0.000	46.111
	NT2RI3006340	19.479	0.000
	NT2RI3006673	11.902	0.000
30	NT2RI3007291	14.928	0.000
	NT2RI3007543	1.012	0.000
	NT2RP7004123	2.289	0.000
	NT2RP7005529	8.006	0.000
	NT2RP7009147	1.900	0.000
35	NT2RP7017474	22.450	0.000
	OCBBF2007028	8.234	0.000

	OCBBF2020741	33.655	0.000
	OCBBF2024850	26.505	0.000
	OCBBF2036743	13.183	0.000
	OCBBF3000483	9.520	0.000
5	PLACE6001185	25.473	0.000
	PLACE7000514	5.673	0.000
	PUAEN2007044	1.710	0.000
	PUAEN2009655	4.359	0.000
	SKNSH2000482	23.251	0.000
10	SPLEN2006122	0.000	18.769
	SPLEN2016554	22.228	0.000
	SPLEN2031547	5.633	0.000
	SPLEN2036932	3.497	0.000
	STOMA1000189	1.865	0.000
15	STOMA2004925	14.912	0.000
	SYNOV2017055	20.136	0.000
	SYNOV4001395	21.660	0.000
	SYNOV4002346	7.153	0.000
	SYNOV4008440	1.759	0.000
20	TCERX2000613	14.497	0.000
	TESOP2002273	4.841	0.000
	TESTI4000014	0.639	0.000
	TESTI4008797	14.824	0.000
	TESTI4009286	2.594	0.000
25	TESTI4012702	2.600	0.000
	TESTI4013675	35.326	0.000
	TESTI4014159	13.979	0.000
	TESTI4018886	64.596	0.000
	TESTI4029671	22.183	0.000
30	TESTI4037156	1.320	0.000
	THYMU2008725	15.552	0.000
	THYMU2031890	21.176	0.000
	THYMU2033070	58.853	0.000
	THYMU2035735	11.014	0.000
35	THYMU3001472	20.097	0.000
	TRACH1000205	4.694	0.000

	TRACH2001443	11.083	0.000
	TRACH2001549	5.043	0.000
	TRACH2005811	1.258	0.000
	TRACH2007834	0.602	0.000
5	TRACH2008300	2.025	0.000
	TRACH3002192	4.463	0.000
	TRACH3003379	29.185	0.000
	TRACH3004068	1.700	0.000
	TRACH3004721	3.467	0.000
10	TRACH3007479	3.848	0.000
	TUTER1000122	0.000	72.738
	TUTER2000425	0.000	100.000
	TUTER2000904	3.330	62.217
	TUTER2000916	0.000	100.000
15	TUTER2001387	0.000	100.000
	TUTER2002729	0.000	100.000
	UTERU1000024	100.000	0.000
	UTERU1000031	100.000	0.000
	UTERU1000148	100.000	0.000
20	UTERU1000249	100.000	0.000
	UTERU1000337	100.000	0.000
	UTERU1000339	100.000	0.000
	UTERU2000649	100.000	0.000
	UTERU2001409	100.000	0.000
25	UTERU2002410	0.700	13.085
	UTERU2002841	64.596	0.000
	UTERU2004688	6.630	0.000
	UTERU2004929	13.845	0.000
	UTERU2005004	41.697	0.000
30	UTERU2005621	5.377	0.000
	UTERU2006115	9.347	0.000
	UTERU2006137	9.269	0.000
	UTERU200656°	100.000	0.000
	UTERU2007444	64.596	0.000
35	UTERU2007520	15.999	0.000
	UTERU2007724	15.672	0.000

	UTERU2008347	100.000	0.000
	UTERU2014678	48.981	0.000
	UTERU2017762	39.037	0.000
	UTERU2019491	100.000	0.000
5	UTERU2019681	100.000	0.000
	UTERU2019706	54.394	0.000
	UTERU2019940	51.819	0.000
	UTERU2020491	100.000	0.000
	UTERU2020718	100.000	0.000
10	UTERU2021163	53.896	0.000
	UTERU2021380	100.000	0.000
	UTERU2022020	100.000	0.000
	UTERU2022981	100.000	0.000
	UTERU2023039	54.394	0.000
15	UTERU2023175	7.103	0.000
	UTERU2023651	29.963	0.000
	UTERU2023712	100.000	0.000
	UTERU2024002	100.000	0.000
	UTERU2024656	51.568	0.000
20	UTERU2025025	100.000	0.000
	UTERU2025645	100.000	0.000
	UTERU2025891	100.000	0.000
	UTERU2026025	100.000	0.000
	UTERU2026090	100.000	0.000
25	UTERU2026203	54.394	0.000
	UTERU2027591	100.000	0.000
	UTERU2029953	100.000	0.000
	UTERU2030213	58.763	0.000
	UTERU2030280	51.819	0.000
30	UTERU2031084	25.928	0.000
	UTERU2031268	100.000	0.000
	UTERU2031521	100.000	0.000
	UTERU2031703	100.000	0.000
	UTERU2031851	100.000	0.000
35	UTERU2033375	1.385	0.000
	UTERU2033382	100.000	0.000

	UTERU2035114	51.568	0.000
	UTERU2035323	100.000	0.000
	UTERU2035328	100.000	0.000
	UTERU2035331	100.000	0.000
5	UTERU2035452	100.000	0.000
	UTERU2035469	100.000	0.000
	UTERU2035503	100.000	0.000
	UTERU2035745	100.000	0.000
	UTERU2036089	100.000	0.000
10	UTERU2037361	100.000	0.000
	UTERU2037577	100.000	0.000
	UTERU2038251	100.000	0.000
	UTERU3000226	62.692	0.000
	UTERU3000645	34.742	0.000
15	UTERU3000665	100.000	0.000
	UTERU3000828	100.000	0.000
	UTERU3000899	33.654	0.000
	UTERU3001059	100.000	0.000
	UTERU3001240	100.000	0.000
20	UTERU3001542	58.853	0.000
	UTERU3001571	51.819	0.000
	UTERU3001572	19.596	0.000
	UTERU3001585	100.000	0.000
	UTERU3001652	100.000	0.000
25	UTERU3001766	54.206	0.000
	UTERU3001988	100.000	0.000
	UTERU3002209	100.000	0.000
	UTERU3002218	51.568	0.000
	UTERU3002383	100.000	0.000
30	UTERU3002667	100.000	0.000
	UTERU3002731	100.000	0.000
	UTERU3002768	100.000	0.000
	UTERU3002786	51.568	0.000
	UTERU3002993	100.000	0.000
35	UTERU3003116	100.000	0.000
	UTERU3003135	39.146	0.000

	UTERU3003178	100.000	0.000
	UTERU3003465	100.000	0.000
	UTERU3003523	100.000	0.000
	UTERU3003776	100.000	0.000
5	UTERU3004523	100.000	0.000
	UTERU3004616	100.000	0.000
	UTERU3004709	51.819	0.000
	UTERU3004992	100.000	0.000
	UTERU3005049	58.853	0.000
10	UTERU3005205	100.000	0.000
	UTERU3005230	58.249	0.000
	UTERU3005460	62.692	0.000
	UTERU3005585	100.000	0.000
	UTERU3005907	15.610	0.000
15	UTERU3005970	62.692	0.000
	UTERU3006008	100.000	0.000
	UTERU3006308	62.692	0.000
	UTERU3007134	100.000	0.000
	UTERU3007419	62.692	0.000
20	UTERU3007640	54.394	0.000
	UTERU3007913	87.049	0.000
	UTERU3008660	100.000	0.000
	UTERU3008671	100.000	0.000
	UTERU3009259	53.896	0.000
25	UTERU3009490	100.000	0.000
	UTERU3009517	54.206	0.000
	UTERU3009690	100.000	0.000
	UTERU3009871	21.605	0.000
	UTERU3009979	100.000	0.000
30	UTERU3011063	100.000	0.000
	UTERU3015086	100.000	0.000
	UTERU3015500	100.000	0.000
	UTERU3016789	100.000	0.000
	UTERU3018081	40.205	0.000
35	UTERU3018154	100.000	0.000
	UTERU3018616	25.167	0.000

	UTERU3018711	86.466	0.000
	ADRG2000042	3.029	0.000
	BRHIP3000017	15.777	0.000
	CTONG2003348	39.037	0.000
5	CTONG2019822	7.755	0.000
	CTONG2020378	19.250	0.000
	CTONG2020411	32.844	0.000
	CTONG2024031	6.165	0.000
	FEBRA2028516	1.364	0.000
10	HCASM2008536	15.228	0.000
	HCHON2000743	7.282	0.000
	IMR322001879	11.495	0.000
	MESAN2005303	9.449	0.000
	NT2RI2009583	0.267	0.000
15	OCBBF2008144	3.440	0.000
	PERIG2007068	5.521	0.000
	SPLEN2039379	10.362	0.000
	TESTI2015626	0.784	7.329
	TESTI4013894	33.408	0.000
20	TUTER2000057	0.000	92.461
	UTERU2004299	100.000	0.000
	UTERU2008040	14.037	0.000
	UTERU2011220	4.669	0.000
	UTERU2019534	100.000	0.000
25	UTERU2021820	29.732	0.000
	UTERU2028734	26.183	0.000
	UTERU2032279	100.000	0.000
	UTERU2033577	100.000	0.000
	UTERU2035978	100.000	0.000
30	UTERU3000402	100.000	0.000
	UTERU3000738	41.697	0.000
	UTERU3001053	100.000	0.000
	UTERU3014791	100.000	0.000
	UTERU3015412	100.000	0.000
35	UTERU3017176	100.000	0.000

The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed the following genes whose expression levels differed between the two.

5

Table 20

	Clone ID	NTONG	CTONG
10	BNGH42007788	0.000	5.734
	BRACE1000186	15.935	0.000
	BRACE2006319	0.000	6.530
	BRACE3010428	0.000	6.396
	BRACE3012364	0.000	7.922
15	BRAMY2020058	0.000	52.028
	BRAMY3002803	0.000	26.873
	BRAWH2001671	0.000	7.082
	BRAWH2014645	0.000	1.969
	BRAWH3002574	0.000	12.314
20	BRCAN2009432	0.000	4.905
	BRCAN2015371	0.000	20.417
	BRCAN2020710	0.000	20.242
	BRHIP2004814	0.000	64.609
	BRHIP3018797	0.000	2.495
25	BRTHA2003461	0.000	4.088
	BRTHA3003490	11.964	0.000
	CTONG1000087	0.000	3.895
	CTONG1000088	0.000	5.442
	CTONG1000288	11.209	84.986
30	CTONG1000302	0.000	100.000
	CTONG1000341	0.000	51.706
	CTONG1000467	0.000	16.004
	CTONG1000488	0.000	100.000
	CTONG1000508	0.000	100.000
35	CTONG1000540	0.000	100.000
	CTONG2000042	0.000	65.252

	CTONG2001877	0.000	100.000
	CTONG2004062	0.000	100.000
	CTONG2006798	0.000	17.972
	CTONG2008233	0.000	8.953
5	CTONG2009423	0.000	64.609
	CTONG2009531	0.000	100.000
	CTONG2010803	0.000	20.971
	CTONG2013178	0.000	35.252
	CTONG2017500	0.000	4.934
10	CTONG2019248	0.000	28.179
	CTONG2019652	0.000	100.000
	CTONG2019704	0.000	62.446
	CTONG2019788	0.000	11.390
	CTONG2019833	0.000	100.000
15	CTONG2020127	0.000	100.000
	CTONG2020522	0.000	42.683
	CTONG2020638	0.000	23.060
	CTONG2020806	0.000	100.000
	CTONG2021132	0.000	100.000
20	CTONG2022153	0.000	100.000
	CTONG2022601	0.000	100.000
	CTONG2023021	0.000	62.680
	CTONG2023512	0.000	100.000
	CTONG2024206	0.000	100.000
25	CTONG2024749	0.000	100.000
	CTONG2025496	0.000	100.000
	CTONG2025516	0.000	100.000
	CTONG2025900	0.000	100.000
	CTONG2026920	0.000	100.000
30	CTONG2027327	0.000	52.760
	CTONG2028124	3.704	0.936
	CTONG2028687	0.000	100.000
	CTONG30000^4	0.000	51.585
	CTONG3000657	0.000	7.226
35	CTONG3000686	0.000	100.000
	CTONG3000707	0.000	100.000

	CTONG3000896	0.000	100.000
	CTONG3001123	0.000	14.616
	CTONG3001370	0.000	65.252
	CTONG3001420	0.000	51.138
5	CTONG3001560	0.000	100.000
	CTONG3002020	0.000	100.000
	CTONG3002127	0.000	62.446
	CTONG3002412	0.000	19.932
	CTONG3002674	0.000	41.611
10	CTONG3003179	0.000	100.000
	CTONG3003483	0.000	100.000
	CTONG3003652	0.000	100.000
	CTONG3003654	0.000	100.000
	CTONG3003737	0.000	100.000
15	CTONG3003905	0.000	36.474
	CTONG3003972	0.000	51.706
	CTONG3004072	0.000	36.356
	CTONG3004712	0.000	100.000
	CTONG3005325	0.000	100.000
20	CTONG3005648	0.000	100.000
	CTONG3005713	0.000	100.000
	CTONG3005813	0.000	72.408
	CTONG3006067	0.000	74.021
	CTONG3006186	0.000	100.000
25	CTONG3006650	0.000	100.000
	CTONG3007444	0.000	100.000
	CTONG3007528	0.000	100.000
	CTONG3007586	0.000	100.000
	CTONG3007870	0.000	100.000
30	CTONG3008252	0.000	100.000
	CTONG3008258	0.000	100.000
	CTONG3008496	0.000	100.000
	CTONG3008566	0.000	100.000
	CTONG3008639	0.000	100.000
35	CTONG3008831	0.000	100.000
	CTONG3008894	0.000	2.708

	CTONG3008951	0.000	100.000
	CTONG3009028	0.000	5.995
	CTONG3009227	0.000	100.000
	CTONG3009239	0.000	5.378
5	CTONG3009328	0.000	44.674
	CTONG3009385	0.000	100.000
	FEBRA2007544	0.000	4.560
	FEBRA2007801	0.000	4.598
	FEBRA2021966	31.791	0.000
10	FEBRA2025427	0.000	9.234
	HCHON2000028	0.000	2.955
	HCHON2001217	0.000	3.877
	HHDPC1000118	0.000	3.904
	HSYRA2008376	11.524	0.000
15	KIDNE2001847	0.000	6.778
	KIDNE2002252	0.000	4.060
	MESAN2006563	0.000	2.572
	NT2RI2008724	0.000	3.421
	NT2RI2018883	0.000	50.616
20	NT2RI3000622	63.099	0.000
	NT2RI3006284	0.000	3.854
	NT2RI3006673	0.000	18.588
	NT2RI3007543	6.253	7.901
	NT2RI3007757	0.000	23.555
25	NT2RP7004123	0.000	3.574
	NT2RP7009147	0.000	2.967
	NT2RP7014005	0.000	10.836
	NTONG2000413	79.538	0.000
	NTONG2003852	49.507	0.000
30	NTONG2005277	100.000	0.000
	NTONG2005969	23.675	0.000
	NTONG2006354	100.000	0.000
	NTONG2007249	100.000	0.000
	NTONG2007517	100.000	0.000
35	NTONG2008088	75.309	0.000
	NTONG2008672	100.000	0.000

	OCBBF2001794	34.843	0.000
	OCBBF2006151	0.000	10.738
	PEBLM2004666	0.000	6.920
	PEBLM2005183	0.000	7.010
5	SPLEN2002467	0.000	6.068
	SPLEN2029912	0.000	6.085
	SPLEN2031547	0.000	2.932
	SYNOV4007671	0.000	1.365
	SYNOV4008440	0.000	2.748
10	TBAES2002197	0.000	28.875
	TESOP2002273	0.000	7.560
	TESTI2009474	0.000	3.763
	TESTI4000014	2.632	0.665
	TESTI4000209	0.000	4.934
15	TESTI4008018	0.000	74.021
	TESTI4009286	0.000	1.350
	TESTI4010851	0.000	1.018
	TESTI4012702	0.000	4.060
	TESTI4013675	0.000	18.389
20	THYMU2031847	0.000	69.076
	THYMU2033308	0.000	26.010
	TLIVE2002690	44.414	0.000
	TRACH2005811	0.000	3.928
	TRACH2007059	0.000	62.446
25	TRACH2025535	0.000	2.163
	TRACH3001427	0.000	1.729
	TSTOM2000553	0.000	12.559
	UTERU2005621	0.000	8.397
	UTERU2017762	0.000	60.963
30	UTERU2023175	0.000	2.773
	UTERU3001572	0.000	6.800
	BLADE2006830	24.778	0.000
	BRHIP3000017	0.000	8.213
	CTONG1000113	0.000	20.967
35	CTONG2003348	0.000	60.963
	CTONG2004000	0.000	100.000

	CTONG2008721	0.000	62.680
	CTONG2015596	0.000	100.000
	CTONG2015633	0.000	100.000
	CTONG2016942	0.000	21.398
5	CTONG2019822	0.000	12.111
	CTONG2020374	0.000	57.889
	CTONG2020378	0.000	30.063
	CTONG2020411	0.000	12.823
	CTONG2020974	0.000	74.021
10	CTONG2024031	0.000	19.255
	CTONG2028758	0.000	29.955
	CTONG3001501	0.000	100.000
	CTONG3002552	0.000	100.000
	CTONG3003598	0.000	100.000
15	CTONG3004550	0.000	100.000
	CTONG3004726	0.000	31.543
	CTONG3009287	0.000	100.000
	FEBRA2008692	0.000	13.709
	FEBRA2028516	0.000	4.261
20	HCHON2000508	2.752	9.042
	NT2RI2009583	4.947	0.833
	NTONG2008093	100.000	0.000
	PERIC2007068	0.000	2.874
	TESOP2007384	44.382	37.388
25	TLIVE2002046	0.000	3.380
	TRACH2000862	0.000	53.910

The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA, or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN, or BRTHA) showed the following genes whose expression levels differed between the two.

Table 21

Clone ID	FCBBF	FEBRA	OCBBF	BRACE	BRAZL	BRAMY	BRAWH	BRCAN	BRCOC	BRHP	BRSSN	BRSTN	BRTHA
ADRG2009146	0.000	0.000	0.000	10.913	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ADRG2012038	0.000	0.000	0.000	1.459	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ADRG2012179	0.000	0.000	17.655	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ASTRO1000009	0.000	0.000	0.000	0.000	0.000	0.000	2.611	0.000	0.000	0.000	0.000	0.000	0.000
ASTRO2003960	0.000	0.000	0.000	17.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ASTRO3000482	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BLADE1000176	0.000	0.000	0.000	16.822	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	24.247
BLADE2001371	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	12.691	0.000	0.000	0.000
BLADE2004089	0.000	0.000	12.311	7.034	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BLADE2008398	0.000	0.000	0.000	4.401	0.000	0.000	12.401	0.000	0.000	18.978	0.000	0.000	13.752
BNGH42007788	5.687	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	3.141	0.000	0.000	0.000
BRACE1000186	0.000	0.000	0.000	1.535	0.000	0.000	4.324	0.000	0.000	2.206	0.000	7.796	0.000
BRACE1000258	0.000	0.000	0.000	68.044	0.000	0.000	31.956	0.000	0.000	0.000	0.000	0.000	0.000
BRACE1000533	8.716	11.762	11.722	11.720	0.000	4.754	11.795	0.000	0.000	9.627	8.780	0.000	5.232
BRACE1000572	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2003639	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2005457	0.000	0.000	0.000	41.512	0.000	0.000	58.488	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2006319	6.477	17.479	8.711	4.977	0.000	3.532	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2008594	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2010489	0.000	0.000	0.000	15.026	0.000	10.665	63.510	0.000	0.000	10.799	0.000	0.000	0.000
BRACE2011747	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2014306	0.000	0.000	0.000	6.909	0.000	0.000	0.000	0.000	34.486	0.000	0.000	17.550	5.398
BRACE2014475	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2014657	0.000	0.000	0.000	76.765	0.000	7.784	15.451	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2015058	24.301	0.000	5.447	6.224	0.000	8.836	0.000	0.000	0.000	8.947	0.000	0.000	19.449
BRACE2015314	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2016981	0.000	0.000	0.000	16.089	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2018762	0.000	0.000	0.000	41.027	0.000	0.000	0.000	0.000	0.000	58.973	0.000	0.000	0.000
BRACE2024627	0.000	0.000	0.000	8.689	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2026836	0.000	0.000	0.000	4.898	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2027258	0.000	0.000	41.974	23.981	0.000	34.044	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2027970	0.000	0.000	0.000	45.981	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2028970	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2029112	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2029849	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

BAMY4000095	0.000	0.000	0.000	0.000	14.721	0.000	33.520	51.759	0.000	0.000	0.000	0.000	0.000
BAMY4000229	0.000	0.000	0.000	25.113	35.650	0.000	0.000	0.000	0.000	0.000	0.000	0.000	39.237
BAMY4000277	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRASW1000125	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.946	0.000
BRAWH1000127	0.000	7.969	3.971	4.538	9.663	0.000	15.983	0.000	0.000	0.000	35.693	0.000	7.090
BRAWH2001395	0.000	0.000	0.000	3.580	2.541	3.037	14.290	10.422	0.000	0.000	12.514	4.546	11.652
BRAWH2001671	0.000	0.000	0.000	8.097	0.000	0.000	7.605	0.000	0.000	0.000	0.000	0.000	12.650
BRAWH2001940	0.000	0.000	0.000	0.000	0.000	0.000	37.398	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2001973	0.000	0.000	0.000	0.000	0.000	0.000	37.398	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2002560	11.923	24.132	24.052	0.000	6.503	0.000	6.454	0.000	0.000	0.000	12.010	11.635	0.000
BRAWH2002761	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2005315	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2007658	0.000	0.000	0.000	0.000	0.000	0.000	58.101	0.000	0.000	0.000	0.000	41.899	0.000
BRAWH2010000	0.000	0.000	0.000	0.000	0.000	0.000	18.745	43.006	0.000	0.000	0.000	0.000	0.000
BRAWH2010084	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2010536	0.000	0.000	0.000	0.000	0.000	0.000	14.718	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2012162	0.000	0.000	0.000	0.000	0.000	0.000	36.060	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2012326	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2013294	0.000	0.000	0.000	13.997	0.000	0.000	39.442	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2013871	0.000	0.000	0.000	0.000	0.000	0.000	37.485	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2014414	0.000	0.000	0.000	0.000	0.000	0.000	54.002	0.000	0.000	0.000	0.000	0.000	9.906
BRAWH2014645	0.000	2.635	6.566	3.751	2.130	0.000	4.228	0.000	0.000	0.000	0.000	0.000	1.172
BRAWH2014662	0.000	0.000	0.000	11.016	0.000	0.000	15.521	0.000	0.000	0.000	0.000	0.000	17.212
BRAWH2014876	0.000	0.000	0.000	7.433	0.000	0.000	10.473	24.026	0.000	0.000	0.000	0.000	58.068
BRAWH2014954	0.000	0.000	0.000	41.512	0.000	0.000	58.488	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2016221	0.000	0.000	0.000	0.000	0.000	0.000	47.417	0.000	0.000	0.000	0.000	0.000	52.583
BRAWH2016439	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2016702	0.000	0.000	0.000	26.193	0.000	0.000	73.807	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH2016724	64.881	0.000	0.000	0.000	0.000	0.000	35.119	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3000078	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3000100	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3000314	0.000	0.000	0.000	0.000	0.000	0.000	71.553	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3000491	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3001326	0.000	0.000	0.000	0.000	0.000	0.000	45.606	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3001475	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000
BRAWH3001891	0.000	0.000	0.000	36.772	0.000	0.000	17.401	0.000	0.000	0.000	0.000	0.000	0.000

